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5;
Query Match 10.6%; Score 77.5; DB 6; Length 1045;
Best Local Similarity 25.9%; Pred. No. 8.7;
Matches 29; Conservative 13; Mismatches 43; Indels 27; Gaps
                                                              52 TGLFGEEDVRFRSAPVYM-----PTVVLRRTPACAGGRSVYTEAY-----VTIPV 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-WHITE ALPINE;
STRAIN-WHITE ALPINE;
Hein W.R., Dudler L., Marston W., Landsverk T., Young A., Avila D.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AR038131; AAB92375.1; -.
HSSP; P10988; 1VVD.
INTERPO; PR00048; sushi; 14.
SMART; SM00032; CCP; 1.
SEQUENCE 1045 AA; 115561 MW; FF58E1A2892C0D59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ovis aries (Sheep).

Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;

Bammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                               PRT; 1045 AA.
                                                                                                                                                      97 GCTCVPEPEKDADSINSSIDKQGAKLLLGPNDAP 130
                                                                                                                                                                                  | | | :| |||
576 ACR--PRPSNGVNSPNSS----
                                                                                                                                                                                                                                                                                                                                                      01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2001 (TrEMBLrel. 16, COMPLEMENT RECEPTOR TYPE 2.
                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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046545
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Search completed: October 5, 2001, 15:23:45 Job time: 190 sec

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73 VLRRTPACAGGRSVYTEAYVTIPVGCTCVPEPEKD--ADSINSSIDKQGAKL 122

474 PICKAAECE----

15 PPTNLRSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTG--LFGEEDVRFRSAPVYMPTV 72

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Amentides P.G., Scherer S.E., Lip P.M., Hoskins R.A., Galle R.F.,
Ramerides P.G., Scherer S.E., Lip P.M., Hoskins R.A., Galle R.F.,
Ramerides P.G., Scherer S.E., Lip P.M., Hoskins R.A., Galle R.F.,
Ramerides P.G., Scherer S.E., Lip P.M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell N.D., Zhang Q., Chen L.X.,
Ramerides P.G., Baxter E.G., Helt G., Champen M., Pfelifer B.D.,
Ramerides R.M., Baster B.G., Helt G., Champen M., Pfelifer B.D.,
Ramerides R.M., Baster B.G., Helt G., Nelson C.R., Miklos G.L.G.,
Ramerides R.Y., Bernan B.P., Bayraktaroglu L., Bassley E.M.,
Ballew R.M., Basu A., Baxendle J., Bayraktaroglu L., Bassley E.M.,
Ballew R.M., Basu A., Baxendle J., Bayraktaroglu L., Bassley E.M.,
Ballew R.M., Basu A., Baxendle J., Bayraktaroglu L., Bassley E.M.,
Ballew R.M., Basu A., Baxendle J., Bayraktaroglu L., Bassley E.M.,
Ballew R.M., Bouck J., Bouck J., Broketein P., Brotchar B.,
Bortchan M.R., Bouck J., Broketein P., Brottler P.,
Burtis K.C., Busam D.A., Bulke C., Davenport L.B., Davies P.,
R. Borkova D., Bolcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunko B.C.,
R.D., Hurrey S., Dahlke C., Perraz C., Ferriar S., Felsischmann W.,
R.D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
R.A. Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
R.M. Hamel B.E., Kodire C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
R. Liu X., Mattei B., Molintosh T.C., Moris J., Moshrefi A.,
R. Muntt S.M., Wolly B., Murphy B., Murphy
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
  455 SPWC----STPRSPRSLVCVVPDVAAFC-----SDWRWLRAPITIPMSLVR--- 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CPAGGR---PADRRFRPPTNLRSVSPWAYRISYDPARYP-----RYLPEAYCLCRGCL 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48; Indels
                                         ---RSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQ 118
                                                                              497 -- ADGLFYPSAFSFTYTPEYSVRP-GHPGVPEPATDADALLESIHQE 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FDF9EFEF14E69957 CRC64;
                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5;
5.8;
                                                                                                                                                                               805 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 78; DB
; Pred. No. 5.8;
14; Mismatches
                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly)
                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE003707; AAF55126.1; -. FlyBase; FBgn0038287; CG18442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          287:2185-2195(2000).
                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2000 (TrEMBLrel. 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.7%
Best Local Similarity 23.4%
Matches 36; Conservative
                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                   CG18442 PROTEIN.
                                       79 ACAGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase;
SEQUENCE
                                                                                                                                                                                                    Q9VFD4;
                                                                                                                                                                               09VFD4
                                                                                                                                        RESULT 14
Q9VFD4
ID Q9VFD4
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                                                                                                             Wilson R., Ainscough R., Aderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Libyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thlerry-Mieg J., Thomas K., Vaudin M., Vaudhan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 K-KIASLLEPQISQOSGSIYIGLHRTPACSKS------PISSSC-----NSM 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 CDAGW----TRFNRPS----GGWCVRVF--PGTYHQPLAESRCQSQGAVLTGVQNQEEA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFRSAPVYMPTVV------LRRTPACAGGRSVYTEAYVTIPVGCTCVPEPEKDADSI 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CPAGGRPADRRFRPPTNLRSVSPWAYRISYDPARYPRYLPEAYCLCRGC-LTGLFGEEDV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 SPWAYRISYDPARYPRYL----PEAYCLCRGCLTGLFGEEDVRFRSAPVYMPTVVLRRTP 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 5; Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 552;
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                                       to the EMBL/GenBank/DDBJ databases.
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EMBL; AL021578; CAA16521.1; -.
Interpro; IPR002909; -.
Pfam; PF01833 TIG; ASSEC4B12237AF43 CRC64;
SEQUENCE 552 AA; 60422 WW; 5E2EC4B12237AF43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24150 MW; DB4C40BFFF904200 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAX-1999 (TrEMBLrel. 10, Created)
01-MAX-1999 (TrEMBLrel. 10, Last sequence update)
01-MAX-2001 (TrEMBLrel. 16, Last annotation update)
DJ453C12.2 (SIMILAR TO TRANSCRIPTION FACTOR RPB-L).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.8%; Score 78.5; Dr
Best Local Similarity 25.4%; Pred. No. 1.2;
Matches 31; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 3.8;
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       552 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.7%; Score 78; 29.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                          DifferPro: IPR001304; --
Pfam; PF00059; lectin_c; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                               MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                       Nature 368:32-38(1994).
EMBL; 282093; CAB05021.1; -.
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Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00034; CLECT;
                      Kershaw J.;
Submitted (NOV-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 AA;
                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 NS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 NS 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                         elegans.
                    Kershaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            095723;
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095723
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8

Gaps

16738 MW; ADB51F438DFB3940 CRC64;

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148 AA;
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"Human RBP-L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Q9UBG7
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Q9XUH9
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Wieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Knappe A., Hiller C., Thurau M., Wittmann S., Hofmann H., Fleckenstein B., Fickenscher H.; "The superantigen-homologous viral immediate-early gene iel4/vsag in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 RSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDVRFRSAPVYMPTVVLRRTPA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
14.7%; Score 107.5; DB 14; Length 151;
Best Local Similarity 31.4%; Pred. No. 0.00063;
Matches 27; Conservative 12; Mismatches 36; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Virol. 71:9124-9133(1997).
EMBL, Y13183; CAA73627.1; -.
SEQUENCE 151 AA; 17189 MW; 49B2C9430C46BE32 CRC64;
                                                                                                                                                                                                                                                                                   no RNA stage; Herpesviridae;
                                                                                                                                                                  Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                herpesvirus saimiri-transformed human T cells.",
                                                                                  151 AA.
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                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---GHNPCPNSFRLEXMLVTVGCTCV 143
                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C-488;
MEDLINE=98037620; PubMed=9371569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                                                          Gammaherpesvirinae; Rhadinovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JAN-1999 (TrEMBLrel. 09, F25D1.3 PROTEIN.
                                                                                                                                     01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 11-NOV-1998 (TrEMBLrel. 08, 11-NERBELEUKIN 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 368:32-38(1994).
EMBL; 273973; CAA98268.1; -
                                                                                                                                                                                                                                                  Saimiriine herpesvirus 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239
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                                                                                                             52 RALCPWDSRVNYQESREPKLIAESVCLCRKSRGSTGAF------CMPIVRKVPILRRV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                         20 RSVSPWAYRISYDPARYPRYLPEAYCLCRGC--LTGLFGEEDVRFRSAPVYMPTVVLRRT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Koyama K., Nakamura Y., Okamura S., Azuma C., Kimura T.;
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                       14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 YRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDVRFRSAPVYMPTVVLRRTPACAGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 520;
   Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36; Indels
                                       35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AB024964; BAA88232.1; -. EMBL, AB026048; BAA86121.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfan; PF01833; TIG; 1.
SEQUENCE 520 AA; 57038 MW; BACF92459A77ACFB CRC64;
                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 ----RSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       471 PSAFSFTYTPEYSVRP-GHPGVPEPATDADALLESIHQE 508
 DB 5;
0.005;
                                                                                                                                                       78 PAC--AGGRSVYTEAYVTIPVGC-TCVPEPEKDA 108
                                                                                                                                                                             :| : | : | : | 104 -SCDRSTGLWNYVRSTELITVGCHSVLPRTQRAA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 79.5; D
Pred. No. 2.4;
                                     17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Mismatches
 Score 99;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Koyama K., Isaka S., Okamura S.; "112-pan.";
 13.6%;
29.8%;
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28.3%;
                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 28.3%,
Local 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 12, (TrEMBLrel. 12, (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                  TRANSCRIPTION FACTOR RBP-L.
Query Match
Best Local Similarity 29.89
Matches 28; Conservative
                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR002909;
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TISSUE=PANCREAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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Lee J., Ho W.-H., Maruoka M., Corpuz R.T., Baldwin D.T., Foster J.S., Goddard A.D., Yansura D.G., Vandlen R.L., Wood W.I., Gurney A.L.; "IL-17E, a Novel Proinflammatory Ligand for the IL-17 Receptor Homolog IL-17Rhl.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 ISYDPARYPRYLPEAYCLCRGCLTGLFGEEDVRFRSAPVYMPTVVLRRTPACAGGRSV-Y 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 PTNLRSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEE-DVRFRSAPVYMPTVVL 74
                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last senotation update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DJ108C2.3 (PUTATIVE NOWEL PROTEIN SIMILAR TO ILL7) (INTERLEUKIN 17
(CYTOTOXIC T-LYMPHOCYTE-ASSOCIATED SERINE ESTERASE 8)) (CYTOTOXIC LYMPHOCYTE-ASSOCIATED ANTIGEN 8, CTLA8)) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 78;
                                                                                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 276:1660-1664(2001).
EMBL; AF305200; AAG40848.1; -.
SEQUENCE 177 AA; 20330 MW; 52D895710CD59871 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            66C3C34E7ACC2790 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.4%; Score 119.5; DB 4; 37.8%; Pred. No. 1.6e-05; tive 13; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 110.5; DB 4
Pred. No. 0.00036;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 RRIPACAGGRSVY ----TEAYVTIPVGCTCV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 YRRP-CHGEKGTHKGYCLERRLYRVSLACVCV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177
                        78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.2%;
31.5%;
                                                                                                                                                                                                                                                                                                                                Submitted (FEB-2000) to the EMBL; AL034343; CAB75300.1;
                                                                                                                                                                                                                                                                                                                                                                                          AA; 8704 MW;
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16,
16,
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                        PRELIMINARY;
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01-MAR-2001 (TrEMBLrel.
INTERLEUKIN 17E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 TEAYVTIPVGCTCV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 QLEKVLVTVGCTCV 70
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Les 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 28; Conserv
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                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Q9H293;
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                        Q9NUE6
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CYTOKINE-LIKE PROTEIN 2CYTO7 (NEURONAL INTERLEUKIN-17 RELATED FACTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuronal expression and evaluation as a candidate for the chromosome 5q-linked form of Charcot-Marie-Tooth disease."; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF184970; AAF01319.1; BEMBL; AF18726; AA644135.1; SEQUENCE 180 AA; 20309 MW; E26F4C72001997C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 TNLRSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDVRFRSAPVYMPTVVLRR 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome
                                                                                                                                                          Lehner J.,
                                                                                                                                                                                                                                                   Moore E.E., Presnell S., Garrigues U., Guilbot A., LeGuern E., Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.; "Identification of a novel IL-17 related factor: Demonstration of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ō
                                                            Euteleostomi;
Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moore E.E., Presnell S., Garrigues U., Guilbot A., LeGuern E., Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.; Identification of a novel IL-17 related factor: Demonstration neuronal expression and evaluation as a candidate for the chromatorial expression to the chromatory of the EMBL/GenBank/DDBJ databases.

BMBL, AF218724; AAG41131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 151; DB 11; Length 111; Pred. No. 1e-08; 8; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 180;
                                                                                                                                                        Presnell S., Gilbert T., Whitmore T., Foster D., Hart C.,
Martinez T., Hoffman R., O'Hara P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                       Martinez T., Hoffman R., O'Hara P.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D1598392981BA867 CRC64;
                                                          Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 173; DB 11;
Pred. No. 7.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 LCPQPPRPGPCRQRVVME----TIAVGCTCI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----TPACAGGRSVYTEAYVTIPVGCTCV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12628 MW;
                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.78;
42.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111
                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 AA;
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Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 39; Conserv
                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                NCBI_TaxID=10090;
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SEQUENCE FROM N.A.

MEDLINE-20105548; PubMed=10639155;

Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P.,
Gurney A.L., Wood W.I.;

"Cloning and Characterization of IL-17B and IL17C, Two New Members of
the IL-17 Cytokine Family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moore E.E., Presnell S., Garrigues U., Guilbot A., LeGuern E., Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.; "Identification of a novel IL-17 related factor: Demonstration of neuronal expression and evaluation as a candidate for the chromosome 5q-linked form of Charcot-Marie-Tooth disease.";
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                                                                                                                                                                                                                   SEQUENCE FROM N.A. Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J., Martinez T., Hoffman R., O'Hara P.; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Carrell J.A., Ebner R.;
A novel cytokine receptor-ligand pair. Identification, molecular
characterization, and in vivo immunomodulatory activity.";
J. Biol. Chem. 275:19167-19176(2000).
                  CYTOKINE-LIKE PROTEIN 2CYTO7 (INTERLEUKIN 20) (INTERLEUKIN 17B) (NEURONAL INTERLEUKIN-17 RELATED FACTOR) (INTERLEUKIN-17 BETA). 2CYTO7 OR IL20.
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDILNE-20317118; Pubmed-10749887;
Shi Y., Ullrich S.J., Zhang J., Connolly K., Grzegorzewski K.
Barber M.C., Wang W., Wathen K., Hodge V., Fisher C.L., Olsen
Ruben S.M., Knyazev I., Cho Y.H., Kao V., Wilkinson K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 174; DB 4; Length 180;
Pred. No. 6e-11;
9; Mismatches 38; Indels
                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang W., Wang J., Cao X.;
"Novel cytokine homology with interleukin-17.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF184969; AAF01318.1; -.
EMBL; AF212311; AAF0875.1; -.
EMBL; AF22098; AAF28104.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF218727; AAG44136.1; -.
EMBL; AF110385; AAG39637.1; -.
SEQUENCE 180 AA; 20437 MW; FIBOBC1446D0B14A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 LCPPPPRTGPCRQRAVMETIAVGCTCI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 -- TPACAGGRSVYTEAYVTIPVGCTCV 101
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(TrEMBLrel. 13, I
(TrEMBLrel. 16, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 23.9%;
1 Similarity 43.7%;
38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                             NCBI_TaxID=9606;
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01-MAY-2000
01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 090XT6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 PAKRRCEVNLQLWLSNKRSLSPWGYSINHDPSRIPADLPEARCLCLGCVNPFTMQEDRSM 138
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       17 TNLRSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDVRFRSAPVYMPTVVLRR 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 PADRRFRPP----TNLRSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDVRF 62
                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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                                                                                                                                                                                                                                                                                                                                                      Length 197;
                                                                                                                                                                  SEQUENCE FROM N.A.

Shang W., He L., Wan T., Yuan Z., Cao X.;

Novel human cytokine CX2 with homology to IL-17.";

submitted (PRR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF144A10; AAG27921.1;

SEQUENCE 197 AA; 21784 MW; BAFBB49F6314A768 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20071 MW; 03D02D60BEC89A51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
NEURONAL INTERLEUKIN-17 RELATED FACTOR (FRAGMENT).
Mesocricetus auratus (Golden hamster).
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                               25.7%; Score 187.5; DB 4; ilarity 40.2%; Pred. No. 2.4e-12; Conservative 11; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.2%; Score 176.5; DB 11; llarity 42.0%; Pred. No. 3.2e-11; Conservative 9; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 RSAPVYMPTVVLRR--TPACAGGRSVYTEAYVTIPVGCTC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 VSVPVFSQVPVRRRLCPPPRPGPCRHRVVMETIAVGCTC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                          CYTOKINE CX2 PRECUSOR.
                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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es 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10036;
                                                                                                                                NCBI_TaxID=9606
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                                                                                                                                                                                                                                                                                                                                                                                          37;
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Q9UHF5;
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Matches
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Gaps

180 AA

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014112 homo sapien
09tyc0 pseudorabie
09vty9 drosophila
09vbp9 drosophila
09ulv9 homo sapien
09tr7 arabidopsis
09r1s7 mus musculu
09r1s7 mus musculu
09r1s7 arabidopsis
09f87 homo sapien
09f87 homo sapien
09f87 homo sapien
09f87 pseudomonas
                                                                                                                                                                                                                                                                                                                         Q9uvm6 coprinus ci
Q9p4u6 emericella
O59104 pyrococcus
O64485 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ij
                                               pseudorabie
                                pseudorabie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-20105548; PubMed=10639155;
Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P.,
Gurney A.L., Wood W.I.;
"Cloning and Characterization of IL-17B and IL17C, Two New Members of
the IL-17 Cytokine Family.";
Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).
EMBL, AFIS2099; AAF28105.1, -
SEQUENCE 197 AA; 21765 MW; BAE0152E18DE7D08 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
1NTERLEUKIN 17C.
Homo saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                              09q3f7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.7%; Score 187.5; DB 4; Length 197; 40.2%; Pred. No. 2.4e-12; Live 11; Mismatches 37; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 TPACAGGRSVYTEA-----YVTIPVGCTCV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9HC75 PRELIMINARY; PRT; Q9HC75; 01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                  Q9FK77
Q9R1S7
Q14010
Q9M210
Q9FG87
Q9FZB0
Q9KZB0
                                            0903F7
014212
09PYC0
09VTX9
09VBP9
09ULV9
                                                                                                                                                                                                                                                    090YX6
036377
092EY6
09UZK6
09YAV7
09UVM6
09P4U6
P72236
008592
Q87073
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10
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Best Local Similarity 40.29
Matches 37; Conservative
 PRELIMINARY;
 Q9P0M4
Q9P0M4;
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ID 09
AC 09
DT 01
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   Q9P0M4
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019778 caenorhabdi
029ubg7 homo sapien
09xubg caenorhabdi
095723 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9p124 chlamydia m
Q48780 arabidopsis
                                                                                                                   (without alignments)
781.722 Million cell updates/sec
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Q9uhf5 homo sapien
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09eqi7 rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ognue homo sapien
Q9h293 homo sapien
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O84019 chlamydia t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9p0m4 homo sapien
Q9hc75 homo sapien
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O46545 ovis aries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                           1 SCPAGGRPADRRFRPPTNLR......SIDKQGAKLLLGPNDAPAGP 133
                                                                                                     ; Search time 22.51 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                               Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                   425026 seqs, 132305027 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                               US-09-320-713-4_COPY_28_160
                                                                                                     October 5, 2001, 15:20:35
                                                                                                                                                                                                                                                                                                                                                                                                    Listing first 45 summaries
                                                                        OM protein – protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09POM4
09HC75
09HC75
09UHF5
09UHF6
09UHF6
09UBC7
09HBC7
09UBC7
09
                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_rodent:*
sp_unclassified:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_organelle:*
sp_phage:*
sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_fung1:*
                                                                                                                                                                                                                                                                                                                                                                                                                                 SPTREMBL_16:*
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114.7
119.9
110.9
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110.7
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110.3
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11:
12:
14:
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187.5
176.5
174
173
173
119.5
110.5
107.5
99
79.5
78.5
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76
75.5
75
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                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                            Sequence:
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RARANTETETES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i-SUBUNT: EACH CLASS OF RNA POLYMERASE IS ASSEMBLED FROM TEN TO TWELVE DIFFERENT POLYPEPTIDES. THE 215 KDA POLYPEPTIDE IS THE LARGEST COMPONENT OF RNA POLYMERASE II.

-i-SUBCELLULAR LOCATION: UNCLEAR.

-i-PTM: THE TANDEM 7 RESIDUES REPEATS CAN BE HIGHLY PHOSPHORYLATED.

THE PHOSPHORYLATION ACTIVATES POLZ.

-i-MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES WERE FOUND IN EURARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conserved structure with an essential function.";
Mol. Cell. Biol. 8:311-329(1988).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
SUBSTRATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-472 FROM N.A.
MEDLINE-85282618; PubMed=2992806;
Biggs J., Searles L.L., Greenleaf A.L.;
"Structure of the eukaryotic transcription apparatus: features of the gene for the largest subunit of Drosophila RNA polymerase II.";
Cell 42:611-621(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Endopterygota, Diptera, Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Allison L.A., Wong J.K.-C., Fitzpatrick V.D., Moyle M., Ingles C.J.; "The C-terminal domain of the largest subunit of RNA polymerase II of Saccharomyces cerevisiae, Drosophila melanogaster, and mammals: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jokerst R.S., Weeks J.R., Zehring W.A., Greenleaf A.L.;
"Analysis of the gene encoding the largest subunit of RNA polymerase II in Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRECURSOR, POLYMERASE II'FOR THE MRNA PRECURSOR, AND POLYMERASE III FOR 5S AND TRNA GENES.
SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                01-NOV-1986 (Rel. 03, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6).
                                                                                                                                                                                                 PRT; 1896 AA
282 YASSGTSLGGSDSPVFEAGVFGPPQPPAAP 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gen. Genet. 215:266-275(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1441-1889 FROM N.A. MEDLINE-88094402; PubMed-3122024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S04457; RNFF2L.
FlyBase; FBgn0003277; RpII215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M27431; AAA28868.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M11798; AAA28863.1; -. EMBL; M19537; AAA28827.1; -.
                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR000684; -...
Interpro; IPR000722; -...
Interpro; IPR002879; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7227;
                                                                                                                                                                                          RPB1_DROME
P04052;
                                                                                                                                                           RPB1_DROME
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        PFGH854; RNA_POL_A2; 1.

        PROSITE: PSO0623; RNA_POL_A1:

        PROSITE: PSO015; RNA_POL_II_REPEAT; 11.

        Transferase; DNA-directed RNA polymerase; Transcription; Zinc; Repeat; DNA-binding; Nuclear protein; Phosphorylation; Zinc-finger.

        ZN_FING
        67
        83
        CARBOXXL_TERMINAL

        DOMAIN
        1581
        1383
        CARROXXL_TERMINAL

        CONFLICT
        450
        F -> G (IN REF. 2).

        CONFLICT
        455
        458
        TLHK -> RCTT (IN REF. 2).

        CONFLICT
        453
        472
        GHRWXVLPWS -> VTGESVASST (IN REF. 2).

        SEQUENCE
        1896 AA; 210045 MW; 801EA661FC0BAD5B CRC64;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1635 PSSSGYSPTSPVYSPTVQFQSSPFRGSGSNIYSPGNAY-----SPSSSNYSPN 1683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1591 SSPGGASP---NYSPSSPNYSPTSP----LYASPRYASTTPNFNPQS-----TGYS 1634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 GEEDVRFRSAPVYMPTVVLRRIPACAG-GRSVYT--EAYVTIPVGCTCVPEPEKDADSIN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SCPAGGRPADRRFRPPT-NLRSVSPWAYRISYDPARY----PRYLPEAYCLCRGCLTGLF 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 1896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.5%; Score 69.5; Dilarity 24.8%; Pred. No. 29; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5, 2001, 15:23:16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 SSIDKQGAKLLLGPNDAPAGP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Search completed: October Job time: 181 sec

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lai W.S., Thompson M.J., Taylor G.A., Liu Y., Blackshear P.J.; "Promoter analysis of Zfp-36, the mitogen-inducible gene encoding the zinc finger protein tristerraprolin."; J. Biol. Chem. 270:25266-25272(1995).
-1- FUNCTION: PROBABLE REGULATORY PROTEIN WITH A NOVEL ZINC FINGER STRUCTION: PROBABLE REGULATING THE RESPONSE TO GROWTH FACTORS. HAS BEEN EXPERIMENTALY SHOWN TO BE ABLE TO BIND ZINC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 VRFRSAPVYMPTVVLRR--TPACAGGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDK 117
                                                                        84 ELPRRGALALGCIALLLIMGIVGCTTVTDGTAMPDTNVAPAYRSSVSASVSASAATSSIRE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --FSAAPGHL----CRRDPTPACCPSCRRATPNSVWGPVGGLA---RSPSAHSLGSDPDE 281
   24 ACCLDGRPPIVPHRRRRRIAALRSVLRMRDTPRPARSRCDQVTSHAVLIGWRAVPRRHGG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRPADRRFR-PPTNLR--SVSPWAYRISYDPARYPRYL---PEAYCLCRGCLTGLFGEED 59
                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                         39 YLPEAYCLCRGC----LIGLFGEEDVR-----FRSAPVYMPIVVLRRTPACAGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat; Metal-binding; Zinc-finger; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47;
                                                                                                            ----RSVYTEAYVTIPVGCTCVPEPEKDA-DSINSSIDKQGAKLLLGPNDAPA 131
                                                                                                                                               144 SQRQQSLTTKA---IRTSCDALAATSKDAIDKVNAYVAAFNQGRNTGPTEGPA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- INDUCTION: BY STIMULATION WITH VARIOUS MITOGENS.
-i- SIMILARITY: CONTAINS 2 CX(8)CX(5)CX(3)H-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51; Indels
                                                                                                                                                                                                                                                                           01-ocT-1996 (Rel. 34, Created)
01-ocT-1996 (Rel. 34, Last sequence update)
01-ocT-2000 (Rel. 40, Last annotation update)
TRISTETRAPROLINE (TTP) (TIS11A PROTEIN) (TIS11) (ZFP-36).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-P-P-G.
CX(8)CX(5)CX(3)H-TYPE.
CX(8)CX(5)CX(3)H-TYPE.
6046057E9EA278EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.0%; Pred. No. 3.9;
tive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.5%; Score 69.5;
                                                                                                                                                                                                                                           324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---QGAKL------LLGPNDAPAGP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-d-d-d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96027638; PubMed=7559666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34087 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L42319; AAB05819.1; -.
InterPro; IPR000571; -.
Pfam; PF00642; zf-CCCH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200
222
126
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Best Local Similarity
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218
107
145
324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nuclear protein;
REPEAT 69
                                                                                                                                                                                                                                       TTP_BOVIN
P53781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
ZN_FING
ZN_FING
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eighmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davisn R., Devlin K., Feltwell T., Gentles S., Hamiln N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares T., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Squares S., Squares R., Sulston J.E., Deciphering the biology of Mycobacterium tuberculosis from the Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --PARYPR 38
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                          33 PARYPRYLPEAYCLCRGCLTG----LFGE--EDVRFRSAPVY-----MPTVVLRRTPAC 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45;
                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.7%; Score 70.5; DB 1; Length 265;
                                                                                                                                                                                   Length 425;
                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                          al protein.
425 AA; 43842 MW; 2A6D733CA149E665 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265 AA; 27529 MW; F9E7ACF3A736B90A CRC64;
                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69;
                                                                                                                                                                                   Score 71.5; DB 1;
Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SCPAGGRP---ADRRFRPPTNLRSV----SPWAYRISYD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL 27.5 KDA PROTEIN RV2240C.
RV2240C OR WITCH27.21C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Pred. No. 2.4;
15; Mismatches
                                                                                                                                                                                                                      9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rv2240c; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98295987; PubMed-9634230;
                                                                                  EMBL; AB007919; BAA32295.1; -.
Hypothetical protein.
SEQUENCE 425 AA; 43842 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 270692; CAA94661.1; -.
                                                                                                                                                                                 Similarity 34.2%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                 384 AGPGSPAAASAWTVSP 399
                                                                                                                                                                                                                                                                                                                             81 AG-GRSVYTEAYVTIP 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tuberculist;
                                                                                                                                                                                 Query Match
Best Local Simi
Matches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         YM40_MYCTU
Q10522;
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ITS ROLE AS AN INHIBITOR OF CELLULAR PROLIFERATION IN RESPONSE TO DNA DAMAGE. MAY BIND TO AND INHIBIT CYCLIN-DEPENDENT KINASE ACTIVITY, PREVENTING PHOSPHORYLATION OF CRITICAL CYCLIN-DEPENDENT KINASE SUBSTRATES AND BLOCKING CELL CYCLE PROGRESSION.
SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   variants of the CIP1/WAF1 gene occur together and are associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell 87:297-306(1996).
-i- FUNCTION: MAY BE THE IMPORTANT INTERMEDIATE BY WHICH P53 MEDIATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94170884; Pubmed-8125163; Noda A., Ning Y., Venable S.F., Pereira-Smith O.M., Smith J.R.; "Cloning of senescent cell-derived inhibitors of DNA synthesis using an expression screen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97015085; PubMed-8861913; Gulbis J.M., Kelman Z., Hurwitz J., O'Donnell M., Kuriyan J.; Structure of the C-terminal region of p21(WAF1/CIP1) complexed with human PCNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jiang H., Fisher P.B.;
"Use of a sensitive and efficient subtraction hybridization protocol for the identification of genes differentially regulated during the induction of differentiation in human melanoma cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDIINE-94081955; Pubmed-8259214;
MATOR V., Hannon G.J., Zhang H., Casso D., Kobayashi R., Beach D.;
Toll 1s a universal inhibitor of cyclin kinases.";
Nature 366:701-704(1993).
                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-94061996; PubMed-8242751;
Harper J.W., Adami G.R., Wei N., Keyomarsi K., Elledge S.J.;
The p21 cdk-interacting protein Cipl is a potent inhibitor of G1
cyclin-dependent kinases.";
Cell 75:805-816(1993).
01-FEB-1995 (Rel. 31, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR I (MELANOMA DIFFERENTIATION
ASSOCIATED PROTEIN 6) (MDA-6) (P21) (CDK-INFERACTING PROTEIN 1).
CDKNIA OR CDKNI OR CIPI OR WAFI OR MDA6 OR SDII OR PICI OR CAP20.
                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                    El-Deiry W.S., Tokino T., Velculescu V.E., Levy D.B., Parsons Trent J.M., Lin D., Mercer W.E., Kinzler K.W., Vogelstein B.; "WaFl, a potential mediator of p53 tumor suppression.";
                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jiang H., Lin J., Herlyn M., Kerbel R.S., Weissman B.E., Welch D.R., Fisher P.B.;
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mousses S., Oezcelik H., Lee P.D., Malkin D., Bull S.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 139-160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Genet. 4:1089-1092(1995).
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MEDLINE-95384154; PubMed-7655464;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an expression screen.";
Exp. Cell Res. 211:90-98(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                              Cell 75:817-825(1993).
                                                                                                 Homo sapiens (Human)
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                                                                                                                                                         NCBI_TaxID=9606;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license(isb-sib.ch).
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-i- TISSUE SPECIFICITY: IS EXPRESSED IN ALL ADULT HUMAN TISSUES, WITH 5-FOLD LOWER LEVELS OBSERVED IN THE BRAIN.
-i- INDUCTION: BY THE P53 TUMOR SUPPRESSOR/ONCOGENE. ALSO BY MEZEREIN (ANTILEUKEMIC COMPOUND) AND BY IFN-BETA.
-i- SIMILARITY: THE N-TERMINAL OF CIPI AND KIP ARE SIMILAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cycle; Nuclear protein; Zinc-finger.

ING 13 41 C4-TYPE (POTENTIAL).

IN 141 156 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

ENCE 164 AA; 18119 MW; 98DIE7C519ADFCA9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 PAG-----GRPADRRFRPPTNLRSVSPWAYRISYDPARYPRYLPEAYCLCRGC----- 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 ------LTGLFGEEDVRFRSAP-VYMPTVVLRRTPACAGGRSVYT-----
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Last annotation update)
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EMBL; L26165; AAA19811.1; -.
EMBL; L47233; AAB59560.1; ALT_INIT.
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MEDLINE-98116662; PubMed-9455484;
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01-0CT-2000 (Rel. 40, Last anno
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KIAA0450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L25610; AAA16109.1; -.
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SWISS-2DPAGE; P38936; HUMAN.
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Best Local Similarity
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EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL)
                                                                                                                                         GAG-ALPHA (GLUCOSAMINOGLYCAN ATTACHMENT
 Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi; Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain; Hyaluronic acid; Alternative splicing.
SIGNAL 13358 VERSICAN CORE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC...)
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                                                                                 IG-LIKE V-TYPE DOMAIN.
LINK 1.
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10; Mismatches
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                                                                                                                                                           DOMAIN).
GAG-BETA.
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                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 270:3914-3918(1995).
-I- FUNCTION: MAY PLAY A ROLE IN INTERCELLULAR SIGNALING AND IN
CONNECTING CELLS WITH THE EXTRACELLULAR MATRIX. MAY TAKE PART IN
THE REGULATION OF CELL MOTILLIY, GROWTH AND DIFFERENTATION. BINDS
                                                                                                                                                                                                                                                                STRAIN-C57BL/6;
MEDLINE-951BL/6;
MEDLINE-951BL/6;
ASHOOMURA T., Ujita M., Ito K., Kimata K.;
Expression of PG-M(V3), an alternatively spliced form of PG-W
without a chondroitin sulfate attachment in region in mouse and human tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -I-SUBCELLULAR LOCATION: SECRETED; EXTRACELLULAR MATRIX.
-I-ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS; V0 (SHOWN HERE), V1,
V2 AND V3; ARE PRODUCED BY ALTERNATIVE SPLICING.
-I-TISSUE SPECIFICITY: V2 IS FOUND ONLY IN BRAIN.
-I-DEVELOPMENTAL STAGE: DISAPPEARS AFTER THE CARTILAGE DEVELOPMENT.
-I-SIMILARITY: CONTAINS 1 IMMUNGLOBULIN-LIKE V-TYPE DOMAIN.
-I-SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
-I-SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-I-SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-I-SIMILARITY: CONTAINS 1 SISHII (SCR) REPEAT.
-I-SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                   STRAIN-C57BL/6, AND SWISS WEBSTER; TISSUE-Brain;
MEDLINE-9512251; PubMed-782236;
Ito K., Shinomura T., Zako M., Ujita M., Kimata K.;
Imultiple forms of mouse PG-M, a large chondroitin sulfate proteoglycan generated by alternative splicing.";
J. Biol. Chem. 270:958-965(1995).
(CHONDROITIN SULFATE PROTEOGLYCAN CORE PROTEIN 2) (PG-M)
                                                                                                                                                                                                                                                          SEQUENCE OF 1-348 AND 3053-3358 FROM N.A. (VARIANT V3)
                                                                                                                     SEQUENCE FROM N.A. (VARIANTS VO; V1 AND V2)
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EMBL; D32040; BAA06802.1; -.
HSSP; P00740; 11XA.
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PROSITE; PSO0010; ASX_HYDROXYL;
PROSITE; PS01186; EGF_1; 2.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01241; LINK; 2.
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Interpro; IPR001881; -.
Fram; PF00008; EF; 2.
Pfam; PF00193; Xlink; 2.
Pfam; PF00193; Xlink; 2.
Pfam; PF000195; Interpro; 
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EGFBLOOD.
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InterPro; IPR000152; -.
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                                                                                                                         Gaps
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071B80026BC0762D CRC64;
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ID CDN1_HUWAN STANDARD;
AC P38936;
DT 01-FEB-1995 (Rel. 31, Created)
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FUNCTION: RECEPTOR FOR COMPLEMENT C3D AND FOR THE EPSTEIN-BARR VIRUS ON HUMAN B-CELLS AND T-CELLS. PARTICIPATES IN B LYMPHOCYTES
                                                 -1-SUBCELLGUAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1-ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; A LONG FORM (SHOWN HERE) AND ITSOHOR FORM; A MATURE B LYMPHOCYTES, T LYMPHOCYTES AND FOLLICULAR DENDRITIC CELLS OF THE SPLEEN.
-1-SIMILARITY: TO MOUSE CR2. CD21 IS A MEMBER OF THE REGULATORS OF COMPLEMENT ACTIVATION (RCA) FAMILY.
-1-SIMILARITY: CONTAINS 15 SUSHI (SCR) DOMAINS.
-1-DATABASE: NAME-PROW: NOTE-CD guide CD21 entry; WHW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd21.htm".
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Pfam: PF00084; sush1; 15.
Complement pathway; Glycoprotein; Transmembrane; Repeat; Signal;
Receptor; Sush1; Alternative splicing.
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PIR; E24319; E24319.
PIR; F24319; F24319.
HSSP; P10998; IVVC.
MIM; 120650; -.
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C24319;
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CHARGE RELAY SYSTEM (BY SIMILARITY).
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Glycoprotein; Blood coagulation; Plasma; Kringle; Serine protease;
Hydrolase; Fibrinolysis; EGF-like domain; Repeat; Zymogen; Signal.
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
HYPOTHETICAL 142.5 KDA PROTEIN C23E2.02 IN CHROMOSOME
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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ALPHA-FACTOR XIIA LIGHT
FIBRONECTIN TYPE-II.
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MEDLINE-86287311; PubMed-3016712;
Weis J.J., Fearon D.T., Klickstein L.B., Wong W.W., Richards S.A.,
"Identyn Kops A., Smith J.A., Weis J.H. Weis J.H.
"Identification of a partial cDNA clone for the C3d/Epstein-Barr
virus receptor of human B lymphocytes: homology with the receptor for fragments C3b and C4b of the third and fourth components of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genomic organization and polymorphisms of the human C3d/Epstein-Barr
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                Walsh S.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterization of the EBV/C3d receptor on the human Jurkat T cell line: evidence for a novel transcript."; J. Immunol. 150:5311-5320(1993).
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01-FEB-1991 (Rel. 17, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
COMPLEMENT RECEPTOR TYPE 2 PRECEPTORSOR (CR2) (COMPLEMENT C3D RECEPTOR)
(EPSTEIN-BARR VIRUS RECEPTOR) (EBV RECEPTOR) (CD21 ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-93294286; PubMed-8390333;
Sinha S.K., Todd S.C., Hedrick J.A., Speiser C.L., Lambris J.D.,
Tsoukas C.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Frazier
              Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                      1273 AA; 142489 MW; 3FEFF6433DF3C0B6 CRC64;
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Fujisaku A., Harley J.B., Frank M.B., Gruner B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 83:5639-5643(1986).
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                                                                                                                                                                                                                                                                                                                      POTENTIAL.
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Pfam; PF01593; Amino_oxidase; 1.
Hypothetical protein; Transmembrane.
TRANSMEM 1028 1048 POTENTI
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                                                                                                                                                                                                                                    EMBL; Z68887; CAA93114.1; -.
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Best Local Similarity 25.6%
Matches 22; Conservative
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P20023;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brown W.M., Christie D.L., Saunders N.R., Nawratil P.,
Dziegielewska K.D., Mueller-Esterl W.;
"The nucleotide and deduced amino acid structures of sheep and pig
fetuin. Common structural features of the mammalian fetuin family.";
Eur. J. Biochem. 205:321-331(1992).
--- SUBCELLULAR IOCATION: SECRETED.
--- SIMILARITY: BELONGS TO THE FETUIN FAMILY.
--- SIMILARITY: CONTAINS 2 CYSTATIN-LIKE DOMAINS.
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BY SIMILARITY.

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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

"TANYED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                  Sus scrofa (P1g).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
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                                                                                                                                                                       01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-027-2000 (Rel. 40, Last annotation update)
ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A) (FRAGMENT).
AHSG OR FETUA.
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532648EE434B5686 CRC64;
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                                                                                                                                  362 AA
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92209519; PubMed-1372866;
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PROSITE; PS01254; FETUIN_1; 1.
PROSITE; PS01255; FETUIN_2; 1.
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Matches 27; Conservative
                                                                                                                                  STANDARD;
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258
353
353
1129
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216
244
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PIR; S22395; S22395
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173
362 AA;
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151 LGRQAAK 157
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DOMAIN
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RA Sembo U.; Yanamoto T.; Kunisada T., Shibuya Y., Tanase S.,
Rabara T., Okabe H.:
Ramaroto T., Kanisada T., Shibuya Y., Tanase S.,
Ramaroto T., Kanamoto T., Kunisada T., Shibuya Y., Tanase S.,
RT Cleavage site differs from the human molecule.";
Biochim. Biophys. Acta 1159:113-121(1992).
CC THE INITIATION OF BLOOD COAGULATION, FIRRINOLYSIS, AND THE GENERATION OF BLOOD COAGULATION, FIRRINOLYSIS, AND THE GENERATION OF BRADYKININ AND ANGIOTENSIN.
CC ATIVATES COAGULATION FACTORS VII AND XI.
CC ATIVATES CAGULATION TO AN ANIONIC SURFACE, PREMELLIREBIN, SIPPRAFORD BY FACTOR XII TO FORM KALLIREBIN, WHICH THEN CLEAVES FACTOR XII TO FORM KALLIREBIN, WHICH THEN CLEAVES FACTOR XII TO FORM KALLIREBIN TO BETA-FACTOR XIIA.
CC XIIA ACTIVATES FACTOR XI TO FACTOR XIA.
CC SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE-I DOMAIN.
CC --- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE-I DOMAIN.
CC --- SIMILARITY: CONTAINS 1 RIBRONECTIN TYPE-II DOMAIN.
CC --- SIMILARITY: CONTAINS 2 RGF-LIKE BOMB STHE
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                                                                                                                                                                                                                                                                                                                                 Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-RNOV-1997 (Rel. 35, Last annotation update)
COAGULATION FACTOR XII PRECURSOR (EC 3.4.21.38) (HAGEMAN FACTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 19-37; 318-332 AND 359-373
----DAGAT----PVVDAAATASPLADVPAASLVVGP 290
                                                                                                                                         603 AA
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FIBRONECTIN_2; 1.
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FIBRONECTIN_1; 1.
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PROSITE: PS00135; TRYPSIN_SER; 1.
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PROSITE; PS00022; EGF_1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRINGLE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X68615; CAA48600.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00051; kringle; 1. Pfam; PF00089; trypsin; 1.
                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00008; EGF; 2.
Pfam; PF00039; fn1; 1.
Pfam; PF00040; fn2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000001; -.
InterPro; IPR000083; -.
InterPro; IPR000561; -.
InterPro; IPR000562; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .nterPro; IPR001254; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS01253;
PS50070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS01186;
                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                        (HAF) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; S01.211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Liver;
                                                                                                                                       FA12_CAVPO
Q04962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
PROSITE;
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EF13F33EDF9D689F CRC64;

150 AA; 16876 MW;

SEQUENCE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: STRONG, TO OTHER MAMMALIAN INTERLEUKIN-17 AND TO HERPESVIRUS SAIMIRI IMMEDIATE EARLY GENE 13 PROTEIN.
CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE FROM MOUSE BUT, ON THE BASIS OF SUBSEQUENT WORK (REF.2 AND REF.3), HAS BEEN SHOWN TO BE OF RAT ORIGIN.
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                       20 RSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDVRFRSAPVYMPTVVLRRTPA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97031826; Pubmed-8877732; Kennedy J., Rossi D.L., Zurawski S.M., Vega F. Jr., Kastelein R.A., Wagner J.L., Hannum C.H., Zlotnik A.; Wander J.L., Hannum C.H., Zlotnik A.; Whouse IL-17: a cytokine preferentially expressed by alpha beta TCR CD4-CD8-T cells."; J. Interferon Cytokine Res. 16:611-617(1996).

I. FORCTION: INDUCES STROMAL CELLS. TO PRODUCE PROINFLAMMATORY AND HEMATOPOLETIC CYTOKINES (BY SIMILARITY).

SUBUNIT: HOMODIMER (BY SIMILARITY).

SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
115-JUL-1998 (Rel. 36, Last annotation update)
INTERLEUKIN-17 PRECURSOR (IL-17) (CYTOTOXIC T LYMPHOCYTE-ASSOCIATED ILITORN (TLA-8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-93294300; PubMed-8390535; Rouvier E., Luciani M.F., Mattei M.-G., Denizot F., Golstein P.; "CTLA-8, cloned from an activated T cell, bearing AU-rich messenger RNA instability sequences, and homologous to a herpesvirus saimiri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . .) (POTENTIAL).
                                       11;
 Length 151;
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-96194901; PubMed-8654948;
Yao Z., Timour M., Painter S., Fanslow W., Spriggs M.K.;
"Complete nucleotide sequence of the mouse CTLA8 gene.";
 DB 1;
                                     37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LINKED (GLCNAC. . -> L (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND ORGANISM IDENTIFICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytokine; Glycoprotein; T-cell; Antigen; Signal.
14.9%; Score 108.5; DB 131.4%; Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERLEUKIN-17.
                                                                                                                                                                                                                                                                         150 AA
                                   11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@lsb-sib.ch).
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I -> L (I)
                                                                                                                                                                   ---GHQPCPNSFRLEKMLVTVGCTCV 143
                                                                                                                                             80 CAGGRSVYTEAY ---- VTIPVGCTCV 101
                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunol. 150:5445-5456(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L13839; AAA37490.1;
                                   Conservative
                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM IDENTIFICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 168:223-225(1996).
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63
46
                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID::10116;
                                 27;
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 Query Match
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                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Miranda-Rios J., Morera C., Taboada H., Davalos A., Encarnacion S., Mora J., Soberon M.;
"Expression of thiamin biosynthetic genes (thicoGE) and production of symbiotic terminal oxidase cb3 in Rhizobium etli.";
J. Bacteriol. 179:6887-6893(1997).
-i. FUNCTION: REQUIRED FOR THE SYNTHESIS OF THE HYDROMETHYLPYRIMIDINE
                                                                                                                                                                                                     57 RPSDYLNRSTSPWTLSRNEDPDRYPSVIWEAQCRHQRCVNA-EGKLDHHMNSVLIQQEIL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 --EDVRFRSAPVYMPTVVLRRTPACA-GGRSVYTEAYVTIPVGCTCVPEPEKDADSINSS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96 KPEDNGFATGERLTPEFPVRNTPLKAKAGRAVTQLAYAR----AGIVTPEMEFIAIREN 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                           Gaps
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                                                                                                                                        14 RPPINL-RSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDVRFRSAPVYMPTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 PAGGRPADRRFRPPTNLRSVSPW---AYRISYDPARYPRYLPEAYCLCRGCLTGLFGE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
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9
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       Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9CE7F560DB35ACDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HMP) MOIETY OF THIAMINE (4-AMINO-2-METHYL-5-
ch 14.8%; Score 108; DB 1; Similarity 34.4%; Pred. No. 0.00013; 31; Conservative 11; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYDROXYMETHYLPYRIMIDINE) (BY SIMILARITY).
-!- PATHWAY: THIAMINE BIOSYNTHESIS.
-!- SIMILARITY: BELONGS TO THE THIC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) THIAMINE BIOSYNTHESIS PROTEIN THIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           610 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Mismatches
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                                                                                                                                                                                                                                                                                                                         116 VLKREPEKCP---FTFRVEKMLVGVGCTCV 142
                                                                                                                                                                                                                                                                                     73 VLRRTP-ACAGGRSVYTEAYVTIPVGCTCV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CE3; MEDLINE=98037482; PubMed=9371431;
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SEQUENCE 610 AA; 67105 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhizobiaceae; Rhizobium.
NCBI_TaxID=29449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002817;
Pfam; PF01964; ThiC;
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   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhizobium etli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
THIC_RHIET
ID THIC_RHIET
AC 034291;
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
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                                                                                                                                 69 RSTSPWNLHRNEDPERYPSVIWEAKCRHLGCINA-DGNVDYHMNSVPIQQEILVLRREPP 127
                                                                              Gaps
                                                                                                         RSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDVRFRSAPVYMPTVVLRRTPA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-BALBAC; TISSUE-Thymocytes;
MEDLINE-97031826; PubMed-8877732;
MEDLINE-97031826; PubMed-8877732;
Magner J., Rossi D.L., Zurawski S.M., Vega F. Jr., Kastelein R.A., Wagner J.L., Hannum C.H., Zlotnik A.;
"Mouse IL-17: a cytokine preferentially expressed by alpha beta TCR CD4-CD8-T cells.";
J. Interferon Cytokine Res. 16:611-617(1996).
                                                                                                                                                                                                                                                                     02336; 060971; Created)
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update).
INTERLEUKIN-17 PRECURSOR (IL-17) (CYTOTOXIC T LYMPHOCYTE-ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- FUNCTION: INDUCES STROMAL CELLS TO PRODUCE PROINFLAMMATORY AND HEMATOPOIETIC CYTOKINES (BY SIMILARITY).
-:- SUBGNIT: HOMODIMER (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: SECRETED.
-:- TISSUE SPECIFICITY: RESTRICTED TO A SUBSET OF ACTIVATED T-CELLS.
-:- TISSUE SPECIFICITY: STRONG, TO OTHER MAMMALIAN INTERLEUKIN-17 AND TO HERPESVIRUS SAIMIRI IMMEDIATE EARLY GENE 13 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090,
N-LINKED (GLCNAC. . .) (POTENTIAL).
2BCAE9CB2F4886D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 158 INTERLEUKIN-17.
71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
158 AA: 17490 MW; 3505C143435F4653 CRC64;
                                                                              5
                                                 Query Match 17.9%; Score 130.5; DB 1; Length 155; Best Local Similarity 37.3%; Pred. No. 5.3e-07; Matches 31; Conservative 8; Mismatches 39; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yao Z., Timour M., Painter S., Fanslow W., Spriggs M.K.; "Complete nucleotide sequence of the mouse CTLA8 gene."; Gene 168:223-225(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytokine; Glycoprotein; T-cell; Antigen; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=129/SV; TISSUE=T-cell; MEDLINE=96194901; PubMed=8654948;
                                                                                                                                                                            128 HCPNS---FRLEKILVSVGCTCV 147
                                                                                                                                                             80 -CAGGRSVYTEAYVTIPVGCTCV 101
68 N
17504 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 12-158 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U35108; AAA93253.1; -. MGD; MGI:107364; I117.
                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                        ANTIGEN 8) (CTLA-8).
IL17 OR CTLA8.
           155 AA;
 68
                                                                                                                                                                                                                                                           IL17_MOUSE
            SEQUENCE
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 CARBOHYD
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                     9
                                                                                                                                         5 GGRPADRRFRPPTNL-RSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDVRFR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-90163221; PubMed-2154888;
Albrecht J.-C., Fleckenstein B.;
"Structural organization of the conserved gene block of Herpesvirus
salmiri coding for DNA polymerase, glycoprotein B, and major DNA
                                                                                                                                                                                                                  64 SAPVYMPTVVLRRTP-ACAGGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGA 120
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDIINE=92333688; PubMed=1321287;
Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Blesinger B.,
Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B.,
Honess R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nicholas J., Smith E.P., Goles L., Honess R.;
"Gene expression in cells infected with gammaherpesvirus salmiri:
"properties of transcripts from two immediate-early genes.";
Virology 179:189-200(1990).
-!- SIMILARITY: STRONG, TO MAMMALIAN INTERLEUKIN-17 (CTLA-8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.

IMMEDIATE EARLY GENE 13 PROTEIN.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

53BEDDE4206C6432 CRC64;
     Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Primary structure of the herpesvirus saimiri genome.";
J. Virol. 66:5047-5058(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herpesvirus saimiri (strain 11).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
     DB 1;
15.6%; Score 113.5; DB 1
31.4%; Pred. No. 3.5e-05;
ive 16; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1992 (Rel. 21, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                            151 AA
                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17180 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  binding protein.";
Virology 174:533-542(1990).
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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PIR; B45351; B45351
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                      Best_Local Similarity
Matches 37; Conserv
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P24916;
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Q16552 homo sapien 061386 mus musculu 05238 mus scrofa 01453 rattus norv 034291 rhizobium e P29700 sus scrofa 004962 cavia porce 01013 schizosacch 05023 homo sapien 07538 homo sapien 07538 homo sapien 07538 homo sapien 07538 homo sapien 0753781 bos taurus P3781 bos taurus P63781 homo sapien 094376 mus musculu P16075 gallus gall 099956 homo sapien 099956 homo sapien 099956 homo sapien 07070 mericella P26996 thermus aqui P49763 homo sapien 067222 aquifex aeo P3740 escherichia 067222 aquifex aeo P3740 escherichia 067222 aquifex aeo P3740 escherichia 06722 aquifex aeo P3740 accobarichia 06722 aquifex aeo P3740 accobarichia 06723 aquifex aeo P3740 accobarichia p90037 bacteriopha P31263 homo sapien P30634 synechococc
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(without alignments)
394.457 Million cell updates/sec
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1 SCPAGGRPADRRFRPPTNLR.....SIDKQGAKLLLGPNDAPAGP
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                      93435 seqs, 34255486 residues
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PCCY_MOUSE
CDN1_HUMAN
Y450_HUMAN
Y440_MYCTU
TTP_BOVIN
RPB1_BROME
MYOB_RHOCA
HXCA_MOUSE
MYOD_CHICK
MYOD_CHICK
MYOD_CHICK
HRA1_REA_HUMAN
HRA1_REA_HUMAN
HRA1_REA_HUMAN
TCF8_MOUSE
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PLGF_HUMAN
STCL_EMENI
YJJN_ECOLI
METK_AQUAE
ACSB_ACEXY
HXA4_MOUSE
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IL17_MOUSE
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IL17_RAT
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FA12_CAVPO
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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113.5
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Q29488 macaca fasc P13611 homo sapien P70671 mus musculu P41969 mus musculu Q27793 trypanosoma Q16974 aplysia cal Q83675 treponema p P79702 cyprinus ca Q42499 fugu rubrip Q03490 mycobacteri P53596 caenorhabdi P22091 mus musculu		LYMPHOCYTE-ASSOCIATED	Craniata; Vertebrata; Buteleostomi; Catarrhini; Hominidae; Homo.	mo L., Ait-Yahia S., land S., Blanchard D., stein P., Banchereau J.,	cells to produce ines.";	Macduff B.M., cells.";	PROINFLAMMATORY AND ACE EXPRESSION OF THE IN FIBROBLASTS.	D MEMORY T-CELLS. COSYLATED FORMS. 3 PROTEIN.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	1.
497 1 CPDH_MACFA 419 1 IRF3_MOUSE 419 1 IRF3_MOUSE 521 1 DRTS_TRYCR 649 1 KPC1_APLCA 649 1 NPTS_TRYCR 640 1	ALIGNMENTS	HUMAN STANDARD; PRT; 155 AA. 016552; NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 101-OCT-2000 (Rel. 40, Last annotation update) NUPERLEGERIN-17 PRECURSOR (IL-17) (CYTOTOXIC T) ANTIGEN 8) (CTLA-8).	Chordata; Primates;	111 SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-96281911; PubMed-8676080; Fossiez F., Djossou O., Chomarat P., Flores-Romo L., Maat C., Pin JJ., Garrone P., Garcia E., Saeland S Gaillard C., Das Mahapatra B., Rouvier E., Golstein I Lebecque S.;	"T cell interleukin-17 induces stromal cells to proinflammatory and hematopoietic cytokines."; J. Exp. Med. 183:2593-2603(1996).	TISSUE-T-cell; TISSUE-T-cell; MEDLINE-96094436; PubMed-7499828; Yao Z., Painter S.L., Fanslow W.C., Ulrich D., Macduff Spriggs M.K., Armitage R.J.; Hunan IL-17: a novel cytokine derived from T cells.";	J. Immunol. 155:5483-5486(1995)!- FUNCTION: INDUCES STROMAL CELLS TO PRODUCE PROMATOPOLETIC CYTOKINES. ENHANCES THE SURRACE INTRACELLULAR ADHESION MOLECULE-1 (ICAM-1) IN	SUBCELLUIA LOCATION: SECRETED. TISSUE SPECIFICITY: RESTRICTED TO ACTIVATED MEMORY T-CELLS. PTW: FOUND BOTH IN GLYCOSYLATED AND NONGLYCOSYLATED FORMS. SIMILARITY: STROKG, TO OTHER MAMMALIAN INTERLEUKIN-17 AND TO HERPESVIRUS SAIMIRI IMMEDIATE EARLY GENE 13 PROTEIN.	y is copyright. It is prodingtitute of Bioinformatics ormatics Institute. There institutions as long as at most is not removed. Ulcense agreement (See htt license@isb-sib.ch).	33.1; 44.1; 23 T-cell; Antigen; Signal POTENITAL. 155 INTERLEUKIN-17.
888888888888		TAN STANI 997 (Rel. 3: 997 (Rel. 4: 0000 (Rel. 4: KIN-17 PRECI	Metazoa; Metazoa; Sutheria;	COM N.A. 181911; Pr Djossou In JJ., Das Mal	erleukin tory and 1. 183:25	OM N.A. 11; 194436; Pourter S.L. (1, Armital)	mmunol. 155:5483-54 FUNCTION: INDUCES S HEMATOPOIETIC CYTOK INTRACELLULAR ADHES	SPECIFIC SUND BOTH SITY: SIR	PROT ent. The Swiss The Bioinf The Profit The Prof	20; CAA91. 59; AAC50 9; -
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Search completed: October
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                                                                                                                                                                         C; Specias: Musicalius (notice mouse)
C; Date: 10. Sep-1999 #sequence_revision 10. Sep-1999 #text_change 10. Sep-1999
C; Accession: A55535
B; Hob. K.; Shinomura, T.; Zako, M.; Ujita, M.; Kimata, K.
J. Biol. Chem. 20. 958-965, 1995
A; Title: Multiple forms of mouse PG-M, a large chondroitin sulfate proteoglycan generate A; Reference number: A55535; MUID: 9512251
A; Recession: A55535; MUID: 9512251
A; Accession: A55535; MUID: 9512251
A; Accession: A55535
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-2397 RESS
A; Cross-references: GB: D16263; NID: 9862460; PIDN: BAA03796.1; PID: 9862461
C; Superfamily: versions: C-type lectin homology; complement factor H repeat homology; EG
F; 1-20/Domain: signal sequence #status predicted AMT>
F; 167-44/Domain: signal sequence #status predicted AMT>
F; 265-346/Domain: link protein repeat homology <LNK1>
F; 265-346/Domain: link protein repeat homology <LNK2>
F; 2131-2294/Domain: C-type lectin homology <LNH>
F; 2131-2294/Domain: C-type lectin homology <LNH>
F; 2298-2354/Domain: complement factor H repeat homology <PHD>
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A;Molocule type: mRNA
A;Cross-references: GB:L47233; NID:9986878; PIDN:AAB59560.1; PID:9986879
B;Harper, J.W.; Adami, G.R.; Wei, N.; Keyomarsi, K.; Elledge, S.J.
A;Hile: The p21 Cdk-interacting protein Cipl is a potent inhibitor of Gl cyclin-depende
A;Reference number: A49437; MUID:94061996
A;Accession: A49437
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N;Alternate names: probable DNA synthesis inhibitor
C;Species: Homo saplens (man)
C;Decies: Homo saplens (man)
C;Decies: Howo saplens (man)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 01-Dec-2000
C;Accession: I68674; A49437; I53412; S39357
R;Mousses, S.; Ozcelik, H.; Lee, P.D.; Malkin, D.; Bull, S.B.; Andrulis, I.L.
Hum. MOI. Genet. 4, 1089-1092, 1995
A;Title: Two variants of the CIPL/WAFI gene occur together and are associated with human A;Reference number: I54380; MUID:95384154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 18-181 <RE3>
A; Cross-references: GB:L25610; NID:g425142; PIDN:AAA16109.1; PID:g425143
R; Noda, A.; Ning, Y.; Venable, S.F.; Pereira-Smith, O.M.; Smith, J.R.
Exp. Cell Res. 211, 90-98, 1994
A;Title: Cloning of senescent cell-derived inhibitors of DNA synthesis using an expressi
A;Reference number: 153412; MUID:94170884
                            N'Alternate names: chondroitin sulfate proteoglycan 2; chondroitin sulfate proteoglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
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A;Molecule type: mRNA
A;Residues: 18-181 <RE2>
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Best Local Similarity 32.1%; Pred. No. 42;
Matches 26; Conservative 10; Mismatches
                                                                                                           Contains: glial hyaluronate-binding protein
                                                                                                                                                        C; Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2129 DFDECHSNPCRNGATCVDGFN 2149
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versican precursor - mouse
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5, 2001, 15:20:33

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64 ERWNFDFVTETPLEGDFAWERVRGLGLPKLYLPTGPRRGRDELGGGRRPGTSPALLQGTA 123
A;Cross-references: GB:L26165; NID:g418017; PIDN:AAA19811.1; PID:g433742
R:Xiong, Y.; Hannon, G.J.; Zhang, H.; Casso, D.; Kobayashi, R.; Beach, D.
Mature 365, 701-704, 1993
A;Title: p21 is a universal inhibitor of cyclin kinases.
A;Reference number: S39357
A;Accession: S39357
A;Accession: S39357
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 18-181 < XIO>
A;Cross: references: GB:S67388; NID:g453134; PIDN:AAB29246.1; PID:g453135
C;Genetics:
A;Gene: CIPI/WAF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 PAGDVRQNPCGSKACRRLFGPVDSEQLS-------RDCDALMAGCIQEAR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 -------LTGLFGEEDVRFRSAP-VYMPTVVLRRTPACAGGRSVYT------ 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 PAG-----GRPADRRFRPPTNLRSVSPWAYRISYDPARYPRYLPEAYCLCRGC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53;
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53;
                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :| : : || || : |: | EDHVDLSLSCTLVPRSGEQAEGSPGGPGDSQGRK 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89 -EAYVTIPVGCTCVPEPEKDAD-SINSSIDKQGAK 121
                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 71.5; D
; Pred. No. 3.6;
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      9.8%;
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Best Local Similarity 25.2'
Matches 39; Conservative
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9

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106 KDADSINSSIDKQGAKLLLGPNDAPA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            579 SNSNSISSNSTSLNPKDVTDPSHIPS 604
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Matches 37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: SPDB:SPAC23E2.02
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Best Local Similarity
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A; Introns: 8/2; 862/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
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hypothetical protein CT016 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C; Species: Chlamydia trachomatis
C; Species: Chlamydia trachomatis
C; Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C; Cacession: A71568
C; Accession: A71568
C; Accession: A71568
C; Accession: A71579, 1998
C; Accession: A71579, MUD: 99000809
C; Accession: A71568
C; Accession: A71570; MUD: 99000809
C; Accession: A71568
C
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 21-Jul-2000
C;Accession: $22395; $22142
R;Brown, W.M.; Dzieglelewska, K.M.; Saunders, N.R.; Christie, D.L.; Nawratil, P.; Muelle Eur. J. Blochem. 205, 321-331, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: 32295; S22142
R; Brown, W. M.; Dzieglelewska, K. M.; Saunders, N.R.; Christie, D.L.; Nawratil, P.; Muelle Bur. J. Blochem. 205, 321142
A; Title: The nucleotide and deduced amino acid structures of sheep and pig fetuin. Common A; Reference number: S22394; MUD: 92209519
A; Accession: S2395
A; Accession: S2395
A; Molecule type: mRNA
A; Residues: 1-362 CBRW
A; Residues: 1-362 CBRW
A; Residues: 1-362 CBRW
C; Superfeantly: alpha-2-HS-glycoprotein
F; 1-15/Domain: sipinal sequence (fragment) #status predicted <SIG>C; Superfeantly: alpha-2-HS-glycoprotein
F; 1-15/Domain: sipinal sequence (fragment) #status predicted <SIG>F; 16-362/Product: fetuin #status predicted <MAT>F; 16-362/Product: carbohydrate (AMT)
F; 16-362/Promain: cystatin homology <CYI>F; 96,153,173/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 362;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
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Best Local Similarity 27.6%; Pred. No. 3.3;
Matches 27; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 75; DB : Pred. No. 2.1;
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25.0%;
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Matches 20; Conserv
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C:Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
C:Accession: S28941
R:Semba. U.; Yamamoto, T.; Shibuya, Y.; Tanase, S.; Kambara, T.; Okabe, Biochim. Biophys. Acta 1159, 113-121, 1992
A;Title: Primary structure of guinea-pig Hageman factor: sequence around the cleavage A;Title: Primary structure of guinea-pig Hageman factor: sequence around the cleavage A;Accession: S28941; MUID: 93003367
A;Accession: S28941
A;Status: preliminary
A;Molecule type: mRNA
A
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A;Experimental source: strain 972h-; cosmid c23E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
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hypothetical protein SPAC23E2.02 - fission yeast (Schizosaccharomyces pombe)
c;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T38292
R;Skethon, J; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. asubmitted to the EMBL Data Library, January 1996
A;Reference number: Z21784
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Mismatches
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Pred. No. 15
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C; Superfamily: psbG protein
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Best Local Simi
Matches 34;
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C; Species: Rhizobium etli
C; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C; Accession: T44254
R; Miranda Rios, J.; Morera, C.; Taboada, H.; Davalos, A.; Encarnacion, S.; Mora, J.; Sob J. Bacteriol. 179, 6887-6893, 1997
A; Title: Expression of thiamin biosynthetic genes (thicogs) and production of symbiotic
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A Molecule type: DNA
A Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-342 <TET>
A; Cross-references: GB: AE002296; GB: AE002160; NID: g7190325; PIDN: AAF39152.1; PID: g719032
A; Experimental source: strain Nigg (MoPn)
A; Genetics:
A; Genetics:
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Mucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39. A;Reference number: A81500; MUID:20150255
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Molecule type: DNA
Residues: 1-509 <STO>
Cross-references: GB:AE002093; NID:g2760830; PIDN:AAB95298.1; GSPDB:GN00139
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                                                                                                                                                                                                                                                                                     Score 76; DB 2; Length 242;
Pred. No. 1.7;
5; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28;
                                                                                                                                                                                                                                                                                                                                                                                                        161 PEPHCNCLHCQIGRIAVEEEDIEVSEEDLTFRSWDI-----
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209 PLNPEEQFNVYLGTPIGCTC 228
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llarity 26.2%;
Conservative
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Best Local Similarity
Matches 21; Conserv
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A; Map position: 2
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Best Local S
Matches 26
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-178 <ARN>
A;Cross-references: GB:AE001778; GB:AE000512; NID:94981757; PIDN:AAD36289.1; PID:9498
A;Experimental source: strain MSB8
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Nature 399, 323-329, 1999
A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A/Reference number: A72200; MUID:99287316
A/Accession: D72281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein TM1214 - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: 11-dun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: D72281
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                   A; Genome: plasmid b
C; Function:
A; Description: involved in the biosynthesis of the pyrimidine moiety of thiamin
C; Superfamily: thiamin biosynthesis protein thiC
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A;Reference number: 222737; MUID:98037482
A;Accession: T44254
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-610 <MIR>
A;Cross-references: EMBL:AF004408; NID:92627325; PIDN:AAC45972.1; PID:92627326
A;Experimental source: strain CB3
A;Genetics:
A;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.4%; Score 75.5; DB 2; Best Local Similarity 29.9%; Pred. No. 5.1; Matches 38; Conservative 14; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 23.1%; Score 75; DB Similarity 23.1%; Pred. No. 1.5; 4; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 IPVG---CTCVPEPEKDADSINSSIDK 117
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conserved hypothetical protein TC0284 [imported] - Chlamydia muridarum (strain Nigg) C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                            PIDN:CAA98268.1; GSPDB:GN00023; CESP:F25D1.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIDN:CAB05021.1; GSPDB:GN00019; CESP:ZK39.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein ZX39.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27843
R;Kershaw, J.
submitted to the EMBL Data Library, November 1996
A;Reference number: 220428
         C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |: :|||
|---CMPIVRKVPILRRV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 CDAGW----TRFNRPS-----GGWCVRVF--PGTYHQPLAESRCQSQGAVLTGVQNQEEA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFRSAPVYMPTVV-----LRRTPACAGGRSVYTEAYVTIPVGCTCVPEPEKDADSI 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 RSVSPWAYRISYDPARYPRYLPEAYCLCRGC--LTGLFGEEDVRFRSAPVYMPTVVLRRT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CPAGGRPADRRFRPPTNLRSVSPWAYRISYDPARYPRYLPEAYCLCRGC-LTGLFGEEDV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Leus
. 0.0038;
. ~ 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: T27843
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
                                                                                                                                                     A; Accession: T21334
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 68; Sco...
29.88; Pred. No. o...
''ve 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 PAC--AGGRSVYTEAYVTIPVGC-TCVPEPEKDA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18; Mismatches
                                                                                                submitted to the EMBL Data Library, June 1996
A; Reference number: Z19408
                                                                                                                                                                                                                                                           A;Residues: 1-148 <WIL>
A;Cross-references: EMBL:273973; P1
A;Experimental source: clone F25D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:282093; EA;Experimental source: clone ZK39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 29.89 tes 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Genetics:
A;Gene: CESP:ZK39.8
A;Map position: 1
A;Introns: 32/1; 52/3; 108/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 31; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-226 <WIL>
                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: CESP:F25D1.3
A;Map position: 5
                                       C; Accession: T21334 R; Kelly, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Introns: 60/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 28
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                                                                                  Submitted to the EMBL Data Library, January 1992
A. Description: Primary structure of the herpesvirus saimiri genome.
A. Description: Primary structure of the herpesvirus saimiri genome.
A. Reference number: A36806
A. Accession: D36807
A. Molecule type: DNA
A. Mol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 26-Aug-1999
B;Rouvier, E: Luciani, M.
J. Immunol. 150, 5445-5456, 1993
A;Title: CTLA-8, cloned from an activated T cell, bearing AU-rich messenger RNA instabil
A;Reference number: 149623; MUD:93294300
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Resiques: 1-150 <RES>
A;Resiques: 1-150 <RES>
A;Cross-references: GB:L13839; NID:9293329; PIDN:AAA37490.1; PID:9293330
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ÷,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 RSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDVRFRSAPVYMPTVVLRRTPA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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A;Residues: 1-151 <NIC>
A;Cross-references: GB:M60286; NID:g331040; PIDN:AAA46156.1; PID:g331042
R;Albrecht, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytotoxic T-lymphocyte-associated antigen 8 precursor - mouse N; Alternate names: immediate-early protein 2 (ORF13) homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: Ctla-8
C;Superfamily: saimiri herpesvirus immediate-early protein 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F25D1.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 108.5; DB 1
Pred. No. 0.00039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 VLKREPEKCP---FTFRVEKMLVGVGCTCV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 VLRRTP-ACAGGRSVYTEAYVTIPVGCTCV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---GHQPCPNSFRLEKMLVTVGCTCV 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 CAGGRSVYTEAY ---- VTIPVGCTCV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 31.4%;
Matches 27; Conservative 11
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Best Local Similarity
Matches 31; Conserva
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(without alignments)
706.500 Million cell updates/sec
                                                                                                                                                                                                                                                                       SCPAGGRPADRRFRPPTNLR.....SIDKQGAKLLLGPNDAPAGP 133
                                                                                                                                   5, 2001, 15:19:50 ; Search time 14.34 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                   219241
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                       219241 seqs, 76174552 residues
                                                                                                                                                                                                                              US-09-320-713-4_COPY_28_160
                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                   October
                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                   Run on:
                                                                                                                                                                                                                              Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:* pir2:* pir3:*

PIR_68:*

Database :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing:

Description	cytotoxic T-lympho		cytotoxic T-lympho	hypothetical prote		conserved hypothet	probable beta-keto	thiamin biosynthes	hypothetical prote	hypothetical prote	ä	coagulation factor	hypothetical prote	versican precursor	cyclin-dependent k	cyclin-dependent k	transcription fact	hypothetical prote				hypothetical prote	prot	probable NADH-ubiq	probable 3-oxoacyl	myogenic factor CM			probable acetyl-Co
SUMMARIES	JC4628	B45351	149623	T21334	T27843	B81719	A84663	T44254	D72281	A71568	S22395	S28941	T38292	A55535	I68674	I54380	T47860	D70778	C69493	RNFF2L	T03122	F75093	A56552	E71017	T00951	A32872	H75564	A39564	855089
DB	7	-	~	7	7	7	7	~	7	7	7	~	7	-	7	7	N	~	7	Н	~	~	~	~	~	~	~	~	01
s Query Match Length	147	151	150	148	226	242	509	610	178	242	362	603	1273	2397	181	181	256	265	816	1896	292	262	342	173	528	298	872	789	2123
å Query Match		14.9			10.8	10.4	10.4	10.4	10.3	10.3	10.3				8.6							9.4	9.4	9.3	9.3			9.5	
Score	113.5	108.5	108	66	78.5	97	75.5	75.5	75	75	75	7	74.5	73	71.5	70.5	70.5	70.5	^	69.5		68.5	æ	68	68	67.5	7	67	29
Result	-	7	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

Immediate-early protein 2 - saimiriine herpesvirus 1 (strain 11)

NyAlternate names: hypothetical protein ORF13

NyAlternate names: saimirii sclureus (common squirrel monkey)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999

C;Accession: B45321, 35800

NyTitle: Gene expression in cells infected with gammaherpesvirus saimiri: properties A;Reference number: A45351, MUID:91021021

A;Molecule type: mRNA

probable transcrip	p63 related protei	delta-crystallin/E	probable CO-induce	DNA ligase (NAD+)	hypothetical UPF00	placental growth f	co-induced hydroge	hypothetical prote	CT016 hypothetical	conserved hypothet	cytokinin-induced	L-iditol 2-dehydro	probable oxidoredu	S-adenosylmethioni	bcsB protein - Ace	
A71079	T49517	JC4934	T51316	A40363	T50444	A41236	D75115	E70671	B86504	A72120	T10064	S56585	A86135	C70399	B43735	ALTGNMENTS
7	~	~	7	7	7	~	~	7	~1	~	~	_	7	~	~	
773	1114	1117	142	929	1316	149	170	210	273	273	329	345	345	376	802	
9.1	9.1	9.1	9.1	9.1	9.0	8.9	8.9	8.9	8.0	8.9	ø.	8.9	8.9	8 6.	8.9	
66.5	66.5	66.5	99	99	65.5	65	65	65	65	65	65	65	65	65	65	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENT

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A Residues: 1-147 < YAO>
A; Residues: 1-147 < YAO>
A; Residues: 1-147 < YAO>
C; Genetics: GB:U35108; NID:g1244499; PIDN:AAA93253.1; PID:g1244500
C; Genetics: A; Genetics: A; Genetics: A; Genetics: G9/2
C; Superfamily: saimiri herpesvirus immediate-early protein 2
C; Keywords: Cytokine; glycoprotein; lymphocyte 6 C; Keywords: Cytokine; glycoprotein; lymphocyte 6 C; Keywords: Cytokine; glycoprotein; Piphocyte 6 SiG>
F; 1-14/Domain: signal sequence #status predicted csiG>
F; 15-14/Tyroduct: Cytotoxic T-lymphocyte associated antigen 8 #status predicted cMAT>
F; 60/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 15.6%; Score 113.5; DB 2, Best Local Similarity 31.4%; Pred. No. 0.00011; Matches 37; Conservative 16; Mismatches 46
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1;
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    Length 408;
                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/09886404

Sequence 7, Application US/09886404

GENERAL INFORMATION:
APPLICANT: Wedlock, Eugene
APPLICANT: Silbiger, Scott M.
APPLICANT: Silbiger, Scott M.
APPLICANT: Bling, Gary S.
APPLICANT: Bling, Shugian
TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof
FILE REFERENCE: 01017/37128B
CURRENT APPLICATION NUMBER: US/09/886,404

CURRENT FILING DATE: 2001-02-1
PRIOR APPLICATION NUMBER: 60/286,159
PRIOR FILING DATE: 2001-03-16
PRIOR PELING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266,159
PRIOR APPLICATION NUMBER: 60/213,125

PRIOR FILING DATE: 2000-06-22

SOFTWARE: PATENTING DATE: 2000-06-22

SOFTWARE: PATENTING DATE: 2000-06-22

SEQ ID NOS: 22

SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 23.9%; Score 174; DB 5; Length 117; Best Local Similarity 43.7%; Pred. No. 3.3e-10; Matches 38; Conservative 9; Mismatches 38; Indels
                                                Indels
                                                                                                                                                                                     77 --TPACAGGRSVYTEAYVTIPVGCTCV------PEPE 105
                                                                                                                                                                                                                  Score 176.5; DB 5;
Pred. No. 7.2e-10;
9; Mismatches 39;
Query Match 24.2%;
Best Local Similarity 40.2%;
Matches 41; Conservative
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ORGANISM: Homo sapiens
US-09-886-404-7
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US-09-886-404-7
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Db 90 LCPPPRTGPCRQRAVMETIAVGCTCI 116

77 -- TPACAGGRSVYTEAYVTIPVGCTCV 101

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Search completed: October 5, 2001, 15:21:23 Job time: 93 sec

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APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
Abplicant: Goddard, Audrey
APPLICANT: U, Hanzhong
APPLICANT: Li, Hanzhong
APPLICANT: BOOM, William I.
TITLE OF INVENTION: IL-17 HOWOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
CURRENT APPLICATION NUMBER: US 09/311,832
PRIOR APPLICATION NUMBER: US 09/311,832
PRIOR FILING DATE: 1998-05-15
SROID NOS: 26
SEQ ID NOS: 26
LENGTH - 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: L. Hanzhong
APPLICANT: L. HowoloGous POLYPEPTIDES AND THERAPEUTIC USES THEREOF
TITLE OF INVENTION: IL-17 HOWOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
TITLE OF INVENTION: LL-17 HOWOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
CURRENT APPLICATION NUMBER: US/09/854,280
CURRENT FILING DATE: 1999-05-14
PRIOR PELING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US 60/085,579
PRIOR APPLICATION NUMBER: US 60/085,579
PRIOR APPLICATION NUMBER: US 60/113,621
PRIOR FILING DATE: 1998-12-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 25.7%; Score 187.5; DB 5; Best Local Similarity 40.2%; Pred. No. 2.8e-11; Matches 37; Conservative 11; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 TPACAGGRSVYTEA-----YVTIPVGCTCV 101
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; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-09-554-280-12
; Sequence 12, Application US/09854280
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: IL17B-Fc fusion US-09-854-280-12
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US-09-854-280-24
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Filvaroff, Ellen
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liu, Ling
APPLICANT: Terreault Jonathan
TITLE OF INVENTION: Methods of Using A Human IL-17 Related Polypeptide To Treat Disea
FILE REPERENCE: P-14089A
CURRENT APPLICANTON NUMBER: US/60/309,936
CURRENT FILING DATE: 2001-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 25.7%; Score 187.5; DB 5 Best Local Similarity 40.2%; Pred. No. 2.6e-11; Matches 37; Conservative 11; Mismatches 37
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40.2%; Pred. No. 2.6e-11;
tive 11; Mismatches 37
PRIOR APPLICATION NUMBER: PCT/USOO/14042
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: PCT/USOO/15264
PRIOR PLING DATE: 2000-06-02
PRIOR FILING DATE: 2000-06-03
PRIOR PLILOGATION NUMBER: PCT/USOO/23522
PRIOR PPLICATION NUMBER: PCT/USOO/23328
PRIOR PLILING DATE: 2000-08-24
PRIOR PLILING DATE: 2000-12-01
PRIOR PPLICATION NUMBER: PCT/USOO/34956
PRIOR PLILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: PCT/USOI/06520
PRIOR APPLICATION NUMBER: PCT/USOI/19692
PRIOR PLILING DATE: 2001-06-01
PRIOR PLILING DATE: 2001-06-01
PRIOR PLILING DATE: 2001-06-01
PRIOR PLILING DATE: 2001-06-29
PRIOR PLILING DATE: 2001-07-09
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SOFTWARE: Patentin version 3.0
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Best Local Similarity 40.2%
Matches 37, Conservative
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; ORGANISM: Homo sapiens
US-60-309-936-2
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US-09-931-836-11
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LENGTH: 197
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PRIOR FILLING DATE: 1999-11-23
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PRIOR FILLING DATE: 1999-10-128
PRIOR FILLING DATE: 1999-10-128
PRIOR FILLING DATE: 1999-01-22
PRIOR PELING DATE: 1999-01-22
PRIOR PELING DATE: 1999-01-23
PRIOR PELING DATE: 1999-03-24
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PRIOR PELING DATE: 1999-04-05
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PRIOR PELING DATE: 1999-04-13
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PRIOR PELING DATE: 1999-05-04
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PRIOR PELING DATE: 2001-05-09
PRIOR PELING DATE: 2001-05-07
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PRIOR PELING DATE: 2001-05-07
PRIOR PELING DATE: 2009-06-07
PRIOR PELING DATE: 2009-06-07
PRIOR PELING DATE: 2009-06-07
PRIOR PELING DATE: 2009-06-07
PRIOR PELING DATE: 2009-07-07
PRIOR PELING DATE: 2009-06-07
PRIOR PELING DATE: 2009-06-0
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PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
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APPLICANT: GUNDANA, FELL I.
APPLICANT: Ban, James
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Abang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: AC105 ENCODING THE SAME
FILE REFERENCE: P3030R1C1
CURRENT APPLICATION NUMBER: 00/095579
PRIOR FILING DATE: 1998-12-15
PRIOR FILING DATE: 1998-12-15
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-12-23
PRIOR FILING DATE: 1998-12-23
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113430
PRIOR PILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/11365
PRIOR APPLICATION NUMBER: 60/11365
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PRIOR APPLICATION NUMBER: PCT/US99/31274
PRIOR APPLICATION NUMBER: PCT/US00/04341
PRIOR APPLICATION NUMBER: PCT/US00/04341
PRIOR APPLICATION NUMBER: PCT/US00/05601
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-02
PRIOR PFLICATION NUMBER: PCT/US00/05841
PRIOR PLILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-11-10
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 2000-12-01
PRIOR PLILNG DATE: 2000-12-02
PRIOR PRILOR DATE: 2000-12-03
PRIOR PLILNG DATE: 2001-12-03
PRIOR PLILNG DATE: 2001-12-03
PRIOR PLILNG DATE: 2001-12-20
PRIOR PLILNG DATE: 2001-12-20
PRIOR PLILNG DATE: 2001-02-28
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GENERAL INFORMATION:
APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eaton, Dan L.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Best Local Similarity 40.2%
Matches 37; Conservative
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US-09-908-827-4
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APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Gurney, Austin
APPLICANT: Wood, William I.
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFERENCE: P138.RRIC2
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                                                                                                                                       APPLICANT: Bazan, J. Fernando
APPLICANT: Bazan, J. Fernando
APPLICANT: Rastelein, Robert A.
TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
FILE PERFENCE: DX0917K
CURRENT APPLICATION NUMBER: US/09/480,297A
CURRENT FILING DATE: 2000-01-10
PRIOR APPLICATION NUMBER: 60/115,506
PRIOR FILING DATE: 1999-01-11
NUMBER OF SEQ ID NOS: 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 25.7%; Score 187.5; DB 5; Best Local Similarity 40.2%; Pred. No. 2.6e-11; Matches 37; Conservative 11; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.7%; Score 187.5; DB 5;
40.2%; Pred. No. 2.6e-11;
Live 11; Mismatches 37;
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CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/311,832
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 26
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                                                                           Sequence 23, Application US/09480297A GENERAL INFORMATION:
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Best Local Similarity 40.2%
Matches 37; Conservative
                                                                                                                          APPLICANT: Gorman, Daniel M.
                                                                                                                                                                                                                                                                                                                                                          ; SEQ ID NO 23
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-480-297A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 197
TYPE: PRT
ORGANISM: Homo sapiens
                                                         -09-480-297A-23
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APPLICANT: Williams, P.Mickey
APPLICANT: WOOG, William
APPLICANT: WOOG, WILLIam
APPLICANT: WOOG, WILLIam
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFERENCE: P138 HTGLIPICI(US)
FILE REFERENCE: P138 HTGLIPICI(US)
CURRENT APPLICATION NUMBER: US/09/908,827
CURRENT FILING DATE: 2001-07-18
FILING DATE: 1999-03-08
APPLICATION NUMBER: PCT/US99/10733
FILING DATE: 1999-05-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-06-15
PRIOR PAPLICATION NUMBER: 60/13,621
PRIOR PAPLICATION NUMBER: 60/131,022
PRIOR FILING DATE: 1999-04-26
PRIOR FILING DATE: 1999-04-26
PRIOR FILING DATE: 1999-06-131,022
PRIOR FILING DATE: 1999-06-18
PRIOR PAPLICATION NUMBER: 60/134,287
PRIOR APPLICATION NUMBER: 60/134,287
PRIOR PELICATION NUMBER: 60/172,096
PRIOR PELICATION NUMBER: 60/172,096
PRIOR PELING DATE: 1999-16-11
PRIOR APPLICATION NUMBER: 60/172,096
PRIOR PELING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 60/213,807
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-01-24
PRIOR PELING DATE: 2000-10-26
PRIOR PELING DATE: 2000-10-25
PRIOR PELING DATE: 1999-08-25
PRIOR PELING DATE: 1999-08-25
PRIOR PELING DATE: 2000-12-20
PRIOR PELING DATE: 2000-12-20
PRIOR PELING DATE: 2001-03-22
PRIOR PELING DATE: 2001-03-20
PRIOR PELING DATE: 2001-03-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/085,579
                                                                                                                                                                                 ; Sequence 4, Application US/09908827; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         Grimaldi,Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VanLookeren, Menno
                                                                                                                                                                                                                                                     APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vandlen, Richard
                                                                                                                                                                                                                                                                                                                      Fong, Sherman
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hillan, Kenneth
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                                                                                                                                                                                                                                                                                                                                                                                           Godowski, Paul
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TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF FILE REFERENCE: P1381R1C2
CURRENT APPLICATION NUMBER: US/09/854,280
CURRENT FILING DATE: 2001-05-10
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-15
PRIOR FILING DATE: 1999-05-15
PRIOR FILING DATE: 1999-05-15
PRIOR FILING DATE: 1999-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR PELICATION NUMBER: US 60/113,621
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 13
LENGTH: 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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GENERAL INFORMATION:
APPLICANT: Mediock, Eugene
APPLICANT: Silbiger, Scott M.
APPLICANT: Silbiger, Scott M.
APPLICANT: Silbiger, Scott M.
APPLICANT: Silbiger, Scott M.
APPLICANT: Jind, Gary S.
APPLICANT: Jind, Shuqian
TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof
TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof
TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof
FILE REFERENCE: 01017/3128B
CURRENT FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 60/266,159
PRIOR APPLICATION NUMBER: 60/266,159
PRIOR APPLICATION NUMBER: 60/213,125
PRIOR PILING DATE: 2001-02-02
PRIOR FILING DATE: 2000-06-22
SPRIOR FILING DATE: 2000-06-22
SOFTWARE: PALENTING OFFE: 2000-06-22
SOFTWARE: PALENTING OFFE: 2000-06-22
SOFTWARE: PALENTIN VOY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 26.5%; Score 193; DB 5; Length 425; Best Local Similarity 36.4%; Pred. No. 1.7e-11; Matches 43; Conservative 15; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: IL-17C-Fc fusion US-09-854-280-13
                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRGANISM: Homo sapiens US-09-886-404-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-886-404-8
                                                                                                                                                                                                                                                                                                              TYPE: PRT
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Sequence 10, Application US/09480297A

GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Bazan, J. Fernando
APPLICANT: Rasteleln, Robert A.
TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
FILE REFERENCE: DX0917K
CURRENT PAPLICATION UNBER: US/09/480,297A
CURRENT PILING DATE: 2000-01-10
FRIOR APPLICATION NUMBER: 60/115,506
PRIOR FILING DATE: 12000-01-10
NUMBER OF SEQ 1D NOS: 34
SOFTWARE PAPLICATION VOIS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SCPAGGRPADRRFRPPTNLRSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
  TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS FILE REFERENCE: DX0917K
CURRENT APPLICATION NUMBER: US/09/480,297A
CURRENT FILING DATE: 2000-01-10
PRIOR APPLICATION NUMBER: 60/115,506
PRIOR FILING DATE: 1999-01-11
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 12
LENGTH: 205
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Pred. No. 4.6e-14;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      12; Indels
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Pred. No. 1.8e-52;
6; Mismatches 12
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GENERAL INFORMATION:
APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Harzhong
APPLICANT: Wood, William I.
                                                                                                                                                                                                                                                                                                                                                      82.4%;
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Best Local Similarity 84.1%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 83.33
Matches 110; Conservative
                                                                                                                                                                                                                                                                ; ORGANISM: Mus musculus US-09-480-297A-12
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US-09-480-297A-10
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                                                                                                                                                                                                                                          TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Datase, J. Fernando
APPLICANT: Bazan, J. Fernando
APPLICANT: Rastelein, Robert A.
TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
FILE REPERENCE: DXO917K
CURRENT APPLICATION NUMBER: US/09/480, 297A
CURRENT FILING DATE: 2000-01-10
PRIOR PPLICATION NUMBER: 60/115, 506
PRIOR FILING DATE: 1999-01-11
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                                                                                                                                                                                                                                                                                                                                                                                 Length 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                              *99.5%; Score 725; DB 5;
ilarity 99.2%; Pred. No. 7.8e-65;
Conservative 0; Mismatches 1
PRIOR APPLICATION NUMBER: PCT/USO0/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/USO0/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: PCT/USO1/06520
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 39
SEO ID NO 8
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Kastelein, Robert A.
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SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gorman, Daniel M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 KLLLGPNDAPAGP 133
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                                                                                                                                                                                                                                                                      ORGANISM: Homo Sapien
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Best Local Similarity
Matches 132; Conserv
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LENGIH: 151
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TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFERENCE: PISSIRICALPICI(US)
CURRENT APPLICATION NUMBER: US/09/908,827
CURRENT PILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: 60/085,579
PRIOR PLICATION NUMBER: 60/13,621
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-04-21
PRIOR FILING DATE: 1999-04-21
PRIOR PLICATION NUMBER: 60/130,232
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-26
PRIOR FILING DATE: 1999-06-09
PRIOR FILING DATE: 1999-06-09
PRIOR FILING DATE: 1999-06-09
PRIOR FILING DATE: 1999-06-09
PRIOR PRICK DATE: 1999-06-09
PRIOR APPLICATION NUMBER: 60/138,387
PRIOR APPLICATION NUMBER: 60/138,387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2001-05-10
APPLICATION NUMBER: PCT/US99/05028
FILING DATE: 1999-03-08
APPLICATION NUMBER: PCT/US99/10733
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FILING DATE: 2000 08-24
APPLICATION NUMBER: PCT/USO0/30873
FILING DATE: 2000-11-10
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FILING DATE: 1999-12-30
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APPLICATION NUMBER: PCT/US00/05841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US00/15264 FILING DATE: 2000-06-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US00/04341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/213, 807
PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 2000-06-24
PRIOR PELICATION NUMBER: 60/244, 072
PRIOR APPLICATION NUMBER: 60/244, 072
PRIOR PILING DATE: 2000-10-26
PRIOR PILING DATE: 1999-05-14
PRIOR PILING DATE: 1999-06-15
PRIOR PILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-08-25
PRIOR PELING DATE: 1999-08-25
PRIOR PELING DATE: 2000-08-25
PRIOR PLING DATE: 2000-08-25
PRIOR PELING DATE: 2000-08-22
PRIOR PELING DATE: 2000-08-22
PRIOR PELING DATE: 2000-08-22
PRIOR PELING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 09/644, 848
PRIOR PELING DATE: 2001-03-20
PRIOR PELING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 09/854, 208
PRIOR PELING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/854, 208
PRIOR PRILING DATE: 2001-05-10
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FILING DATE: 1999-12-23
APPLICATION NUMBER: 60/175,481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2000-01-11
APPLICATION UNDBER: 60/191,007
FILING DATE: 2000-03-21
APPLICATION NUMBER: 60/213,807
                                                                                 VanLookeren, Menno
Vandlen, Richard
                                                                                                                                   Watanabe, Colin
Williams, P.Mickey
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                                                       Tumas, Daniel
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                                                                                                                                   APPLICANT:
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Sequence 3, Appl
Sequence 2, Appli
Sequence 14, Appl
Sequence 6, Appli
Sequence 34, Appl
Sequence 31, Appl
Sequence 16, Appl
Sequence 25, Appl
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Sequence 59731, A
Sequence 1267, Ap
Sequence 50536, A
                                                                              Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence B, Application US/09480297A

Sequence B, Application US/09480297A

Sequence B, Application US/09480297A

Sequence B, Application Daniel M.

APPLICANT: Gorman, Daniel M.

APPLICANT: Bazan, J. Fernando

APPLICANT: Kastelein, Robert A.

TITLE OF INVENTION: PURITIED MAMMALIAN CYTOKINES; RELATED REAGENTS

FILE REFERENCE: DX0917K

CURRENT APPLICATION NUMBER: US/09/480,297A

CURRENT FILING DATE: 2000-0-10

PRIOR APPLICATION NUMBER: 60/115,506

PRIOR FILING DATE: 1999-01-11

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin version 3.1

FEMALE.
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                      US-09-886-404-10

US-09-886-404-10

US-09-886-404-4

US-09-480-297A-18

US-09-480-297A-12

US-09-886-404-2

US-09-886-404-2

US-09-886-404-2

US-09-886-404-2

US-09-886-385-2

US-09-480-297A-14

US-09-480-297A-16

US-09-480-297A-16
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Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
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APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Shermen
APPLICANT: GodGard, Audrey
APPLICANT: GodGwski, Paul
APPLICANT: Grimaldi, Christop
APPLICANT: Grimaldi, Christop
APPLICANT: Grimaldi, Christop
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CRGANISM: Homo sapiens
US-09-480-297A-8
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Sequence 4, Appli
Sequence 2, Appli
Sequence 12, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 1, Appli
Sequence 1, Appli
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Sequence 4, Appli
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                                                                                                                                                                                             (without alignments)
377.498 Million cell updates/sec
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Sequence 8, Al
Sequence 6, Al
Sequence 12,
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Sequence 13,
Sequence 8, A
Sequence 23,
                                                                                                                                                                                                                                                                                                                    1 SCPAGGRPADRRFRPPTNLR.....SIDKQGAKLLLGPNDAPAGP 133
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3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
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6: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
                         GenCore version 4.5
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US-09-908-827-8

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US-09-886-404-8

US-09-886-404-3

US-09-884-280-3

US-09-884-280-3

US-09-934-2

US-09-934-2

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US-09-854-280-12

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US-09-864-404-7

US-09-929-404-150

US-09-929-404-150

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US-09-886-404-5
US-09-480-297A-33
US-09-854-280-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                           309837 seqs, 47258215 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                       US-09-320-713-4_COPY_28_160
                                                                                                                                                                    5, 2001, 15:19:50
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                      OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                           Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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                                                                                                                                                                      October
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155.5
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LENGTH: 186
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US-09-154-817-3
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                                               Length 186;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Presenal, Scott R.
APPLICANT: Taft, David W.
TITLE OF INVENTION: Mammalian Transforming Growth Factor Beta
FILE REFERENCE: 98-54
CURRENT APPLICATION NUMBER: US/09/397,846B
CURRENT FILING DATE: 2001-05-21
                                                                      Indels
                                            100.0%; Score 729; DB 15;
100.0%; Pred. No. 1.7e-73;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 729; DB 17; Best Local Similarity 100.0%; Pred. No. 1.7e-73; Matches 133; Conservative 0; Mismatches 0;
                                              Query Match
Best Local Similarity 100.0
Matches 133; Conservative
                                                                                                                                                                                                    121 KLLLGPNDAPAGP 133
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US-09-397-846-4
; ORGANISM: Homo sapiens
US-09-154-817-4
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GENERAL INFORMATION:
APPLICANT: Presnell. Scott
APPLICANT: Foley, Kevin
TITLE OF INVENTION: Transforming Growth Factor Beta - 9;
FILE REFRENCE: 98-54X
CURRENT APPLICATION NUMBER: US/09/154,817
CURRENT FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 729; DB 15; Best Local Similarity 100.0%; Pred. No. 1.7e-73; Matches 133; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                   100.0%; Score 729; DB 17;
100.0%; Pred. No. 1.7e-73;
iive 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/100,706
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5, 2001, 15:22:57
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Best Local Similarity 100.0
Matches 133; Conservative
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US-09-154-817-3
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Job time: 187 sec
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US-09-397-846-5
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     Length 173;
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GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Taft, David W.
APPLICANT: Toley, Kevin P.
TITLE OF INVENTION: Mammalian Transforming Growth Factor Beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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APPLICANT: Taft, David
APPLICANT: Foley, Kevin
TITLE OF INVENTION: Transforming Growth Factor Beta
FILE REFERENCE: 98-54X
CURRENT APPLICATION NUMBER: US/09/154,817
CURRENT FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
Query Match 100.0%; Score 729; DB 21; Best Local Similarity 100.0%; Pred. No. 1.5e-73; Matches 133; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.7e-73;
iive 0; Mismatches 0;
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CURRENT FILING DATE: 1999-09-17
EARLIER APPLICATION NUMBER: 60/100,706
EARLIEN FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 185
                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09154817 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 133; Conservative
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ORGANISM: Homo sapiens
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US-09-154-817-5
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LENGTH: 185
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US-09-154-817-5
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US-09-397-846-5
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                                                                                                                                                                                                                              113 RFRSAPVYMPTVVLRRTPACAGGRSVYTEAYVIIPVGCTCVPEPEKDADSINSSIDKQGA 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Taft, David W.
APPLICANT: Taft, David W.
TITLE OF INVENTION: Mammalian Transforming Growth Factor Beta
FILE REFERENCE: 98-54
CORRENT APPLICATION NUMBER: US/09/397,846B
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/100,706
PRIOR APPLICATION NUMBER: 60/100,706
NUMBER OF SEQ ID NGS: 22
SOFTWARE: FastSEO for Windows Version 3.0
               Length
                                                              Indels
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APPLICANT: Taft, David
APPLICANT: Taft, David
APPLICANT: Foley, Kevin
FILE OF INVENTON: Transforming Growth Factor Beta
FILE REFERENCE: 98-54X
CURRENT APPLICATION NUMBER: US/09/154,817
CURRENT FILING DATE: 1998-09-17
SOFTWARE FESQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
  Score 729; DB 17;
Pred. No. 1.7e-73;
• wismatches 0;
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APPLICANT: Presnell, Scott R.
100.0%; Scc
100.0%; Pre
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            Query Match 100.
Best Local Similarity 100.
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                  121 KLLLGPNDAPAGP 133
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Best Local Sim
Matches 133;
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US-09-320-713-32
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LENGTH: 173
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LENGTH: 173
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HUman Genome Sciences, Inc.
TILLE OF INVENTION: INTERLEUKINS-21 AND 22;
FILE REFERENCE: PE470PCT
CURRENT APPLICATION NUMBER: PCT/US99/11644
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: 60/087, 340
EARLIER APPLICATION NUMBER: 60/099, 805
EARLIER APPLICATION NUMBER: 60/090, 805
EARLIER APPLICATION NUMBER: 60/090, 805
EARLIER APPLICATION NUMBER: 60/131, 965
EARLIER FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PALENTIN VET. 2.0
SEQ ID NO 32
                                                         1999-04-30

MBER: PCT US99/11644

1999-05-27
      60/099,805
                                          60/131,965
PRIOR APPLICATION NUMBER: 60/099, PRIOR FILING DATE: 1998-09-10 PRIOR FILING DATE: 1999-04-30 PRIOR FILING DATE: 1999-04-30 PRIOR FILING DATE: 1999-05-27 PRIOR FILING DATE: 1999-05-27 SOFTWARE: PAtentin version 3.0
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US-09-731-816-4
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PCT-US99-11644-32
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                                                                                                                                                           SEQ ID NO 4
LENGTH: 160
TYPE: PRT
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61 RFRSAPVYMPTVVLRRTPACAGGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGA 120
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100.0%; Pred. No. 1.5e-73;
iive 0; Mismatches 0;
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Reinhard Edner
TITLE OF INVENTION: INTERLEUKINS-21 AND 22
FILE REFERENCE: PF470
CURRENT APPLICATION NUMBER: US/09/320,713
CURRENT APPLICATION NUMBER: 60/087,340
EARLIER FILING DATE: 1998-05-29
EARLIER FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: 60/099,805
EARLIER APPLICATION NUMBER: 60/099,805
EARLIER APPLICATION NUMBER: 60/131,965
EARLIER APPLICATION NUMBER: 60/131,965
SEARLIER APPLICATION NUMBER: 60/131,965
SEARLIER FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 32
NUMBER OF SEQ ID NOS: 32
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APPLICANT: Ruben, Steven
TITLE OF INVENTION: Interleukins-21 and 22
TITLE REFERENCE: PF470P1
CURRENT APPLICATION NUMBER: US/09/731,816
CURRENT FILING DATE: 1099-12-09
PRIOR PRILING DATE: 1999-12-09
PRIOR PRILING DATE: 1999-05-27
PRIOR PRILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 60/099,805
PRIOR APPLICATION NUMBER: 60/099,805
PRIOR APPLICATION NUMBER: 60/131,965
PRIOR APPLICATION NUMBER: 60/131,965
PRIOR APPLICATION NUMBER: POT US99/11644
PRIOR APPLICATION NUMBER: POT US99/11644
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; GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.0
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Best Local Similarity 100.
Matches 133; Conservative
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US-09-731-816-32
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RFRSAPVYMPTVVLRRTPACAGGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGA 120
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                                                                      28 SCPAGGRPADRRFRPPTNLRSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDV 87
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       Mismatches
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CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: 60/087,340
EARLIER FILING DATE: 1998-05-29
EARLIER FILING DATE: 1998-05-09
EARLIER FILING DATE: 1998-09-10
EARLIER PILING DATE: 1998-09-10
EARLIER RILING DATE: 1998-09-10
EARLIER FILING DATE: 1999-04-30
NUMBER OF SEO ID NOS: 32
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CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 06/169,837
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-05-27
PRIOR PLICATION NUMBER: 09/320,713
PRIOR PLICATION NUMBER: 60/087,340
PRIOR PILING DATE: 1998-05-27
                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09320713
GENERAL INFORMATION:
APPLICANT: Reinhard Ebner
APPLICANT: Steven M. Ruben
TITLE OF INVENTION: INTERLEUKINS-21 AND 22
FILE REFERENCE: PF470
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GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
APPLICANT: Ruben, Steven
TITLE OF INVENTION: Interleukins-
FILE REFERENCE: PF470P1
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    Matches 133; Conservative
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US-09-320-713-4
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US-09-320-713-4
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LENGTH: 160
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Pred. No. 1.4e-73;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: EDDER, Reinhard
TITLE OF INVENTION: Interleukin-20
FILE REFERENCE: PF399P1
CURRENT APPLICATION NUMBER: US/09/231,788A
CURRENT FILING DATE: 1999-01-15
EARLIER APPLICATION NUMBER: 60/052,870
EARLIER FILING DATE: 1997-07-16
EARLIER FILING DATE: 1997-07-16
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-09-26
EARLIER PILING DATE: 1997-09-26
EARLIER PILING DATE: 1997-09-26
EARLIER PILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PALENTIN VEY: 2.0
SEQ ID NO 12
LENGTH: 160
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TITLE OF INVENTION: INTERLEUKINS-21 AND 22
FILE REFERENCE: FF47OPCT
CURRENT PEPLICATION NUMBER: PCT/US9/11644
CURRENT FILING DATE: 1999-05-27
EARLIER PELING DATE: 1999-05-27
EARLIER PELING DATE: 1999-05-29
EARLIER PELING DATE: 1999-05-29
EARLIER FILING DATE: 1998-05-39
EARLIER FILING DATE: 1998-09-10
EARLIER FILING DATE: 1998-04-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTING OF SEQ ID NOS: 32
LENGTH: 160
                                                                                                                                     Sequence 4, Application PC/TUS9911644 GENERAL INFORMATION:
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148 KLLLGPNDAPAGP 160
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PCT-US99-11644-4
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; ORGANISM: Homo sapiens
US-09-231-788-12
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Sequence 12, Applisequence 9, Applisequence 37, Applisequence 21, Applisequence 12, Applisequence 13, Applisequence 13, Applisequence 23, Applisequence 24, Applisequence 2, Applisequence 4, Applisequence 6, App
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100.0%; Score 729; DB 1;
Best Local Similarity 100.0%; Pred. No. 1.4e-73;
Matches 133; Conservative 0; Mismatches 0;
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TITLE OF INVENTION: Interleukin-20
FILE REFERENCE: P7399PCT2
CURRENT APPLICATION NUMBER: PCT/US00/00807
GURRENT FILING DATE: 2000-01-14
EARLIER APPLICATION NUMBER: 09/231,788
SARALIER FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 29
SOFFWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SERGID NO 12
LENGTH: 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
PCT-US00-00807-12
PCT-US00-00807-12
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Sequence 12, Appl
Sequence 4, Appli
Sequence 32, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 5, Appli
Sequence 5, Appli
                                                                                                                                                (without alignments)
337.749 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                        1 SCPAGGRPADRRFRPPTNLR......SIDKQGAKLLLGPNDAPAGP 133
                                                                                                                              87.36 Seconds
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                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                              ; Search time
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PCT-US99-11644-4
US-09-321-788-12
US-09-320-713-4
US-09-320-713-4
US-09-31644-32
US-09-320-713-32
US-09-731-816-32
US-09-31-816-32
US-09-397-846-5
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                                                                                                                                                                                                                                                                                                                                      2803329 seqs, 221847457 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                         US-09-320-713-4_COPY_28_160
                                                                                                                              October 5, 2001, 15:19:50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Listing first 45 summaries
                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pending_Patents_AA_Main:*
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Maximum DB seq length: 2000000000
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14.9%; Score 108.5; DB 3; Length 151;
Best Local Similarity 31.4%; Pred. No. 3.3e-05;
Matches 27; Conservative 11; Mismatches 37; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       80 CAGGRSVYTEAY----VTIPVGCTCV 101
121 --GHQPCPNSFRLEKMLVTVGCTCV 143
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ. ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDMINES: not relevant
TOPOLOGY: linear
NOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENNE: NO
ORIGINAL SOURCE:
ORGANISM: Herpesvirus Saimiri
STRAIN: ORF13
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Search completed: October 5, 2001, 15:20:11 Job time: 21 sec

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20 RSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDVRFRSAPVYMPTVVLRRTPA 79
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US-09-022-696-8
; Sequence 8, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
14.9%; Score 108.5; DB 3; Length 151;
Best Local Similarity 31.4%; Pred. No. 3.3e-05;
Matches 27; Conservative 11; Mismatches 37; Indels 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: WA
ZIP: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SUSTWARE: Microsoft Word for Apple, Version 6.0.1
APPLICATION NUMBER: US/09/022,696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ---GHQPCPNSFRLEKMLVTVGCTCV 143
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
FREFERNCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 CAGGRSVYTEAY ---- VTIPVGCTCV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                                                                                                                                                                                                                                                                               HYPOTHETICAL: NO
ANTI-SPRE: NO
ORIGINAL SOURCE:
ORIGINAL Herpesvirus Saimiri
STRAIN: ORF13
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NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08
                                                                                                                                                                                                                                     not relevant
                                                                                                                TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
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CLASSIFICATION:
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US-09-022-255-8
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
14.9%; Score 108.5; DB 3; Length 151;
Best Local Similarity 31.4%; Pred. No. 3.3e-05;
Matches 27; Conservative 11; Mismatches 37; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/0902255
Patent No. 6072033
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFLATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15262
TELECOMMUNICATION INFORMATION:
TELEPRONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/034,810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/022,255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 --- GHQPCPNSFRLEKMLVTVGCTCV 143
                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,239
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-034-810-6
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COUNTRY: US
ZIP: 98101
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US-09-022-255-8
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Gaps

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
                         APPLICATION NUMBER: US/08/620,694A
                                                                                                                                                                                           FILING DATE: ... 435
CLASSIFICATION: 435
ATTONEY AGENT INFORMATION:
NAME: PERKINS, PAITIGIA ANDER REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-TELECOMMUNICATION INFORMATION:
                                       21 MARCH 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jacobs, Kenneth
Kelleher, Kerry
Carlin, McKeough
Goldman, Samuel
Pittman, Debra
Mi, Sha
                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 151 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (206)
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Cambridge
STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Giannott
APPLICANT: Golden'F
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Jacobs,
APPLICANT: Kelleher
APPLICANT: Carlin,
                                       FILING DATE: 21
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; STRAIN: (
US-08-620-694A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-034-810-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 GGRPADRRFRPPTNL-RSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDVRFR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 15.4%; Score 112; DB 4; Length 158; Best Local Similarity 33.3%; Pred. No. 1.4e-05; Matches 33; Conservative 14; Mismatches 44; Indels
                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 SAPVYMPTVVLRRTP-ACAGGRSVYTEAYVTIPVGCTCV 101
                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FALLING DATE: 23 MARCH 1995
CLASSIFICATION:
ATCHNEY FAGNT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (206)587-0430
                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/022,257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08620694A Patent No. 5869286 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/620,694
: 51 University Street
Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (20b)
INPORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-09-022-257-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 98101
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                          USA
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                                                                             98101
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                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
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Glannotti, Johnn
Golden'Fleet, Margaret
VENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins
                                                                                                                                                                                                                             20 RSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDVRFRSAPVYMPTVVLRRTPA 79
                                                                                                              Length 151;
                                                                                                              DB 2;
                                                                                                            Query Match 14.9%; Score 108.5; DB 2 Best Local Similarity 31.4%; Pred. No. 3.3e-05; Matches 27; Conservative 11; Mismatches 37
                                                                                                                                                                                                                                                                                                                               121 --- GHQPCPNSFRLEKMLVTVGCTCV 143
                                                                                                                                                                                                                                                                                 80 CAGGRSVYTEAY ---- VTIPVGCTCV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Genetics Institute,
87 CambridgePark Drive
: Herpesvirus Saimiri
ORF13
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 6, Application US/09034810 ; Patent No. 6043344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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58 GAKVSSR--RPSDYLNRSTSPWTLHRNEDPDRYPSVIWEAQCRHQRCVNA-EGKLDHHMN 114
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Sequence 7, Application US/09022257

Patent No. 6197525

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin

APPLICANT: Sprigs, Melanie

APPLICANT: Fanslow, William

TITLE OF INVENTION: No. 6197525e1 Receptor That Binds IL-17

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSE: Immunex Corporation
                                                                                                     APPLICANT: Yao, Zhengbin
APPLICANT: Sprigs, Melanie
APPLICANT: Sprigs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 15.4%; Score 112; DB 4; Length 158; Best Local Similarity 33.3%; Pred. No. 1.4e-05; Matches 33; Conservative 14; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOSTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/022,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 SAPVYMPTVVLRRTP-ACAGGRSVYTEAYVTIPVGCTCV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION:
FILING APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRION.
APPLICATION.
FILING DATE: 23 ...
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PATRICIA ANNE
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (206)587-0430
TELECOMMUNICATION INFORMATION:
TELECHONE: (206)587-0430
TOTAL COORDINATION:
TELECOMMUNICATION:

                                                                                                                                                                                                                                                                                                                E: Immunex Corporation
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
Sequence 7, Application US/09022259
Patent No. 6191104
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-09-022-259-7
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3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                   Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 98101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
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       5 GGRPADRRFRPPTNL-RSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDVRFR 63
                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09022260
Patent No. 6100235
CENERAL INFORMATION:
APPLICANT: You Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.4%; Score 112; DB 3; Length 158; 33.3%; Pred. No. 1.4e-05; tive 14; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
APPLICATION DATA:
APPLICATION NUMBER: US/09/022,260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 SAPVYMPTVVLRRTP-ACAGGRSVYTEAYVTIPVGCTCV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 SAPVYMPTVVLRRTP-ACAGGRSVYTEAYVTIPVGCTCV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFCATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PATLICIA Anne
REGISTRATION NUMBER: 34.695
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
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US-09-022-259-7
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US-09-022-260-7
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Matches 33; Conserve
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; MOLECULE TYPE:
US-09-022-253-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                                                                                                                                    US-09-022-253-7
     US-09-022-696-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                              Length 158;
                                                                                                                                                                                                                                                                               44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,696
                                                                                                                                                                                                                                                                                                                                                                                                            64 SAPVYMPTVVLRRTP-ACAGGRSVYTEAYVTIPVGCTCV 101
                                                                                                                                                                                                                                           15.4%; Score 112; DB 3;
33.3%; Pred. No. 1.4e-05;
tive 14; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
PAPPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09022696 Patent No. 6072037
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (206)587-0430
(206)
                                                                                                                                                                                                                                                                               Conservative
                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acids
TYPE: amino acid
                                                                                                                                                                 ; MOLECULE TYPE: protein US-09-022-255-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                    inear
                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                         (206)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98101
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                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-09-022-696-7
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5 GGRPADRRFRPPTNL-RSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDVRFR 63
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                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09022253
Patent No. 6096305
GENERAL INFORMATION:
APPLICANT: Yea, Zengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
Query Match 15.4%; Score 112; DB 3; Length 158; Best Local Similarity 33.3%; Pred. No. 1.4e-05; Matches 33; Conservative 14; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.4%; Score 112; DB 3; Length 158; 33.3%; Pred. No. 1.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA

COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
CORRATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                  64 SAPVYMPTVVLRRTP-ACAGGRSVYTEAYVTIPVGCTCV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US/08/620,694
FILING DATE: 21-MARCH-1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33; Conservative
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USSN 08/538,765
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                                                                                                                                                                                                                                                     TELEFAX: (206)
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acids
                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-620-694A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seattle
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STREET: 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08620694A
Patent No. 5869286
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
Annercem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 163;
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patent: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 21.3%; Score 155.5; DB 3; Best Local Similarity 36.0%; Pred. No. 1.3e-10; Matches 41; Conservative 15; Mismatches 41;
                                  ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: BLOWN, SCOTT A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15262
TELEPHONE: (617) 498-8224
TELEPHONE: (617) 498-824
TELEPHONE: (617) 496-5651
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LEWGTH: 163 anino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694A
FILING DATE: 21 MARCH 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein US-08-685-239-2
                  CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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5 GGRPADRRFRPPTNL-RSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDVRFR 63
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Patent No. 6072033
GENERAL INFORMATION:
APPLICANT: You Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION:
NOWNER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
15.4%; Score 112; DB 2; Length 158;
Best Local Similarity 33.3%; Pred. No. 1.4e-05;
Matches 33; Conservative 14; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
OPERATING SYSTEM: Apple Operating System 7.5.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 SAPVYMPTVVLRRTP-ACAGGRSVYTEAYVTIPVGCTCV 101
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PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
APPLICATION PROBRE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                          USSN 08/410,535
APPLICATION NUMBER: USSN 08/538,76
FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,53
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
RESISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Immunex Corporation
51 University Street
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Kelleher, Kerry
Carlin, McKeough
Goldman, Samuel
Pittman, Debra
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Best Local Similarity 36.0.
Local 41; Conservative
                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                       Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-09-034-810-2
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                                                                                                                                                                                                                       Cambridge
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APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                      COUNTRY:
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36 SCPPVPGGSMKLDIGIINENQRVSMSRNIESRSTSPWNYTVTWDPNRYPSEVVQAQCRNL 95
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                                                     49 GCLTGLFGEEDVRFRSAPVYMPTVVLRRTPACAGGRSV-YTEAYVTIPVGCTCV 101
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                                                                                                                                              Sequence 12, Application US/08833823
Patent No. 5969093
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: McCoy, John
APPLICANT: McCoy, John
TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
TITLE OF INVENTION: BNCODED THEREBY
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,823 FILING DATE: 10-APR-1997 CLASSIFICATION: 530 CLASSIFICATION DATA:
APPLICATION NUMBER: 08/514,014 FILING DATE: 11-AUG-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.3%; Score 155.5; DB 2; 36.0%; Pred. No. 1.2e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09034810
Patent No. 5043344
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: GIT
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Brown, Scott A. REGISTRATION NUMBER: 32,724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 153 amino acids
TYPE: amino acid
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Best Local Similarity 36.0%
Matches 41; Conservative
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MOLECULE TYPE: protein
US-08-833-823-12
                                                                                                                                    US-08-833-823-12
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US-09-034-810-2
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APPLICANT: Mi, Sha
APPLICANT: Neben, Steven
APPLICANT: Glannotti, Joann
APPLICANT: Golden'Fleet, Margaret
APPLICANT: Golden'Fleet, Margaret
TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neben, Steven
Glannotti, JoAnn
Golden Fleet, Margaret
VENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.3%; Score 155.5; DB 3; Length 163; 36.0%; Pred. No. 1.3e-10; ive 15; Mismatches 41; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 GCLTGLFGEEDVRFRSAPVYMPTVVLRRTPACAGGRSV-YTEAYVTIPVGCTCV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/034,810
                                                                                                                                                                                            ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Brown, Scott A.
REGISTRATION UNDBER: 32,724
REFERENCE/DOCKET UNDBER: GIS28
TELECOMMUNICATION INFORMATION:
TELEPHOR: (617) 896-824
TELEFAX: (617) 876-5821
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 163 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08685239 Patent No. 6074849 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jacobs, Kenneth
Kelleher, Kerry
Carlin, McKeough
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Pittman, Debra
Mi, Sha
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Sequence 2, Appli
Sequence 1, Appli
Sequence 13, Appl
Sequence 13, Appl
Sequence 12, Appli
Sequence 290, App
Sequence 290, App
Sequence 27, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 3, Appli
Sequence 2, Appli
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Sequence 2, Ap
Patent No. 5514
Sequence 4, Ap
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APPLICANT: Jacobs, Kenneth
APPLICANT: McCOy, John
APPLICANT: McCOy, John
APPLICANT: Carlin, McKeough
TITLE OF INVENTION: ENCODED THEREBY
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/514,014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 21.3%; Score 155.5; DB 1; Best Local Similarity 36.0%; Pred. No. 1.2e-10; Matches 41; Conservative 15; Mismatches 41;
US-08-574-043A-2
US-08-524-218A-2
US-08-754-218A-2
PCT-US92-10904-2
PCT-US94-109700-2
PCT-US94-112836-2
PCT-US96-11886A-2
5514582-36
US-08-137-045-13
US-09-138-930-290
US-09-188-930-192
US-09-188-930-192
US-09-188-930-192
US-09-188-930-332
US-09-188-930-332
US-09-188-930-332
US-09-188-930-332
US-08-465-221-2
US-08-465-221-2
                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge STATE: Massachusetts COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DCOKET NUMBER: G16000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEPAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                              Sequence 12, Application US/08514014 Patent No. 5707829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 153 amino acids
amino acid
  ; MOLECULE TYPE: protein US-08-514-014-12
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  FILING DATE:
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US-08-514-014-12
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                                                                               2001, 15:19:50 ; Search time 12.19 Seconds (without alignments) 224.653 Million cell updates/sec
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Sequence 12, Appl
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Sequence 8, 2
Sequence 8, 2
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Sequence 6, 3
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Sequence 9,
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Sequence 8,
Sequence 8,
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Sequence 6,
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-034-810-2
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US-09-022-253-7
US-09-022-259-7
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions, or degenerative conditions. The IL-171 protein can be used in kits and assay methods for identifying compounds that selectively bind to IL-171.
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205 AA; Seguence

ij 4; Gaps Query Match

82.4%; Score 601; DB 21; Length 205;
Best Local Similarity 83.3%; Pred. No. 4.5e-60;
Matches 110; Conservative 6; Mismatches 12; Indels

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121 KLLLGPNDAPAG 132

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Search completed: October 5, 2001, 15:20:59 Job time: 69 sec

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New DNA sequence encoding a mammalian homolog of CTLA-8, designated interleukin-171 (IL-171), useful for recombinant production of IL-171 which can be used for treating conditions associated with abnormal
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                 "protein kinase C phosphorylation site"
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                                              "mature protein"
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/note= "
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/note=
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                               Protein
   1;
                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents an interleukin-173 (IL-173) polypeptide. The polypeptide is an IL-17-like (CTLA-8 related) protein. It is a member of a new group of interleukins, IL-170 polypeptides. The members comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170 protein can be used to treat abnormal proliferation e.g. cancer or degenerative conditions. Antibodies can be used in diagnostic methods to detect over production of IL-170 protein in cells or body
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RFRSAPVYMPTVVLRRTPACAGGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interleukin; IL-171; cytokine; CTLA-8; IL-17; IL-175; IL-173;
IL-174; IL-176; IL-177; cell proliferation; cancer; ss.
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                                                                                                                                                                                                                                                                                                                           polynucleotide encoding a mammalian Interleukin-17 like to identify genes for homologous proteins \cdot
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                                                          /note= "calcium phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 601; DB 21;
Pred. No. 4.5e-60;
6; Mismatches 12;
 "phosphorylation site"
                              /note= "N-glycosylation site"
166..168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1..24
/note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     murine interleukin-173 polypeptide
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                                                                                                                                                                                                                                                 Kastelein RA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.4%;
ilarity 83.3%;
Conservative
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               164..166
   /note=
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193 klllgpadrpag 204
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N-PSDB; AAA58985.
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Best Local Similarity
Matches 110; Conserv
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                                                                                         WO200042188-A2
              Modified-site
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                                                                                                                                                                                                                                                                                                                           New isolated
protein used
                                                                                                                                                                                   11-JAN-1999;
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Peptide
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Claim 6; Page 89; 97pp; English.

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                                                                                                                The present sequence represents an interleukin (IL)-173 polypeptide. It is a mammalian homologue of the cytokine designated CTLA-8 (also referred to as IL-17. The specification also describes homologues IL-17. IL-172, IL-173, IL-173, IL-174, IL-176, and IL-177. The DNA sequence encoding IL-171 is useful for identifying genes, mRNA and sequence encoding IL-171 is useful for identifying genes, mRNA and coDNA molecules which code for related or homologous proteins. The IL-171 protein, antibodies against IL-171, and compounds which have binding affinity to IL-171 are useful in treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions, or degenerative conditions. The IL-171 protein can be used in kits and assay methods for identifying compounds that selectively bind to IL-171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine transforming growth factor beta-9; Ztgf beta-9; Alzheimer's disease; neurodegenerative disease; Huntington's disease; amyofrophic lateral sclerosis; ALS; Parkinson's disease; peripheral neuropathy; demyelinating disease; multiple sclerosis; antiviral; cytostatic.
              interleukin-171 (IL-171), useful for recombinant production of IL-171 which can be used for treating conditions associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mature murine transforming growth factor beta-9, Ztgfbeta-9 protein.
 New DNA sequence encoding a mammalian homolog of CTLA-8, designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotides encoding a novel transforming growth factor beta-9 polypeptide, designated Ztgf beta-9, useful as an antiviral and antiproliferative agent -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 151;
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                                                                                                                                                                                                                                                                                                                                                                                                       DB 21;
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Pred. No. 1.4e-61;
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                                                                                    Disclosure; Page 97; 111pp; English.
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99.18;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                  151 AA;
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                                                                                                 The present sequence is the mature murine transforming growth factor beta-9, designated Ztgf beta-9. The signal sequence extends from amino acid residues 1 to 22. Murine Ztgf beta-9 was found to be highly expressed in the HCL hypothalamic cell line. This can be used to treat a variety of neurodegenerative diseases such as amyotrophic lateral sclerosis (ALS), Alzehimer's disease, Huntington's disease; Parkinson's disease and peripheral neuropathies, or demyelinating diseases including multiple sclerosis. Ztgf beta-9 peptides have antiviral activity and may also be used to regulate the proliferation, differentiation and apoptosis of neurons, glial cells, lymphocytes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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IL-177; IL-171; cell proliferation; cancer.
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Pred. No. 3.9e-60;
6; Mismatches 12;
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Modified-site

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The present sequence represents an interleukin-173 (IL-173) polypeptide. The polypeptide is an IL-17-11ke (CTLA-8 related) protein. It is a member of a new group of interleukins. IL-170 polypeptides. The members comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170 protein can be used to treat abnormal proliferation e.g. cancer or degenerative conditions. Antibodies can be used in diagnostic methods to detect over production of IL-170 protein in cells or body
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interleukin; IL-171; cytokine; CTLA-8; IL-17; IL-175; IL-172; IL-173;
IL-174; IL-176; IL-177; cell proliferation; cancer.
                                                                                                                                                                          New isolated polynucleotide encoding a mammallan Interleukin-17 like protein used to identify genes for homologous proteins -
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SCPAGGRPADRRFRPPTNLRSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.1%; Score 613; DB 21; Length 151; 99.1%; Pred. No. 1.4e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                Claim 11; Page 12-13; 111pp; English.
                                                                                                          Kastelein RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kastelein RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB07690 standard; Protein; 151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A rat interleukin-173 polypeptide.
                             10-JAN-2000; 2000WO-US00006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-JAN-2000; 2000WO-US00005.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                          Gorman DM, Bazan JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bazan JF,
                                                                                (SCHE ) SCHERING CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SCHE ) SCHERING CORP
                                                                                                                                  WPI; 2000-466130/40.
N-PSDB; AAA58982.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-476060/41.
N-PSDB; AAA59156.
                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 111; Conser
                                                                                                                                                                                                                                                                                                                                                               151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200042187-A1
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                                                      11-JAN-1999;
    20-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gorman DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB07690;
                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB07690
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                                                                                                                                                                                                                                                                                                                                The present sequence is a variant of human transforming growth factor beta-9, designated 2tgf beta-9. Human 2tgf beta-9 was isolated from an arrayed pituitary gland cDNA plasmid library by PCR Screening. This can be used to treat a variety of neurodegenerative diseases such as amyotrophic lateral sclerosis (ALS), Alzheimer's disease, Huntington's disease, Parkinson's disease and peripheral neuropathies, or demyelinating diseases including multiple sclerosis. Ztgf beta-9 peptides have antivital activity and may also be used to regulate the proliferation, differentiation and apoptosis of neurons, glial cells, lymphocytes, hematopoietic cells and stromal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RFRSAPVYMPTVVLRRTPACAGGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SCPAGGRPADRRFRPPTNLRSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interleukin; IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;
IL-177; IL-171; cell proliferation; cancer.
                                                                                                                                                                                                                                                     Polynucleotides encoding a novel transforming growth factor beta-9 polypeptide, designated 2tgf beta-9, useful as an antiviral and antiproliferative agent -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 209;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 729; DB 21;
Pred. No. 1.6e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human interleukin (IL) 173 polypeptide.
                         /label= Signal_peptide
 Location/Qualifiers
                                                                                                                                                                                                                                                                                                       Claim 6; Page 92-93; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB07594 standard; Protein; 151 AA.
                                                                                                                                                                                      Foley KP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                        99WO-US21677
                                                                                                                                  98US-0154817
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Best Local Similarity 100.
Matches 133; Conservative
                                                                                                                                                             (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                      Taft DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 KLLLGPNDAPAGP 133
                                                                                                                                                                                                               WPI; 2000-271436/23.
N-PSDB; AAZ52201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200042188-A2
                                                   WO200015798-A2
                                                                                                                                                                                      Presnell SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                        17-SEP-1999;
                                                                             23-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
  Key
Peptide
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99WO-US21677.
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                                                                                                                              (ZYMO ) ZYMOGENETICS INC.
 16..202
                                                                                                                                                     Taft DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 KLLLGPNDAPAGP 133
                                                                                                                                                                          WPI; 2000-271436/23.
N-PSDB; AAZ52195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 133; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                            202 AA;
                                  WO200015798-A2
                                                                                                                                                     Presnell SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
                                                                                17-SEP-1999;
                                                                                                       17-SEP-1998;
                                                          23-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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  Protein
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                                                                                                                                                                                                                   The present sequence represents an interleukin (IL)-173 polypeptide. It is a mammalian homologue of the cytokine designated CTLA-8 (also referred to as IL-17. The specification also describes homologues IL-172, IL-172, IL-173, IL-173, IL-174, IL-176, and IL-177. The DNA sequence encoding IL-171 is useful for identifying genes, mRNA and sequence encoding IL-171 is useful for identifying genes, mRNA and IL-171 protein, antibodies against IL-171, and compounds which have binding affinity to IL-171 are useful in treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions, or degenerative conditions. The IL-171 protein can be used in kits and assay methods for identifying compounds that selectively bind to IL-171.
                                                                                                                                      New DNA sequence encoding a mammalian homolog of CTLA-8, designated interleukin-171 (IL-171), useful for recombinant production of IL-171 which can be used for treating conditions associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RFRSAPVYMPTVVLRRTPACAGGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alzheimer's disease, neurodegenerative disease; Huntington's disease; amyotrophic lateral sclerosis; ALS; Parkinson's disease; peripheral neuropathy; demyelinating disease; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 729; DB 21; Length 202;
Pred. No. 1.5e-74;
Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human transforming growth factor beta-9, 2tgfbeta-9 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human transforming growth factor beta-9; Ztgf beta-9;
                                                                                                                                                                                                 Disclosure; Page 16-17; 111pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..15
/label= Signal_peptide
                                                                              Kastelein RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY70653 standard; Protein; 202 AA.
                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; S
llarity 100.0%; P
Conservative 0;
          10-JAN-2000; 2000WO-US00005
                                  99US-0229402
                                                                                                                                                                          physiology or development -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 KLLLGPNDAPAGP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiviral; cytostatic.
                                                                              Gorman DM, Bazan JF,
                                                       (SCHE ) SCHERING CORP
                                                                                                    WPI; 2000-476060/41.
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 133; Conserv
                                                                                                                                                                                                                                                                                                                                                                        202 AA;
                                                                                                                N-PSDB; AAA59155
                                  11-JAN-1999;
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The present sequence is the human transforming growth factor beta-9, designated 2tgf beta-9. Human 2tgf beta-9 was isolated from an arrayed pituitary gland cDNA plasmid library by PCR screening. This can be used to treat a variety of neurodegenerative diseases such as amyotrophic lateral sclerosis (ALS). Alzheimer's disease, Huntington's disease, Parkinson's disease and peripheral neuropathies, or demyelinating antiviral activity and may also be used to regulate the proliferation, differentiation and apoptosis of neurons, glial cells, lymphocytes, hematopoietic cells and stromal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RFRSAPVYMPTVVLRRTPACAGGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKOGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polynucleotides encoding a novel transforming growth factor beta-9 polypeptide, designated 2tgf beta-9, useful as an antiviral and antiproliferative agent -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SCPAGGRPADRRFRPPTNLRSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDV
/note= "Mature transforming growth factor beta-9"
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lilarity 100.0%; Pred. No. 1.5e-74;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Foley KP;
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130 rfrsapvymptvvlrrtpacaggrsvyteayvtipvgctcvpepekdadsinssidkgga 189
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IL-174; IL-176; IL-177; cell proliferation; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                              'note= "cAMP protein kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "cAMP protein kinase phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                       /note= "mature protein"
                                                                                                                                                                                                     A human interleukin-173 polypeptide.
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                       AAB07689 standard; Protein; 202 AA.
                                                                                                                                                                                                                                                                                                                                /note= "signal
                                                                                                                                                                            (first entry)
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113..116
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166..168
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/note= '
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/note=
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                            KLLLGPNDAPAGP 133
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                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                    AAB07689;
                                                                                                                                                                                                                                                                                                                  Peptide
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         RFRSAPVYMPTVVLRRTPACAGGRSVYTEAVVTIPVGCTCVPEPEKDADSINSSIDKQGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SCPAGGRPADRRFRPPINLRSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDV 60
                                                                                                                                                                                                                                                                       Interleukin; IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;
IL-177; IL-171; cell proliferation; cancer.
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                                                                                                                                                                                                                                            A human interleukin (IL) 173 polypeptide.
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/note= "signal peptide"
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                                                                KLLLGPNDAPAGP 133
                                                                            Bazan JF,
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                                                                                          120
                                                                                                                   Human transforming growth factor beta-9; 2tgf beta-9;
Alzheimer's Alseases, neurodegenerative disease; Huntington's disease;
amyotrophic lateral sclercsis, ALS; Parkinson's disease;
peripheral neuropathy; demyelinating disease; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mature human transforming growth factor beta-9, Ztgfbeta-9 protein-1.
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                        RFRSAPVYMPTVVLRRTPACAGGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGA
1 SCPAGGRPADRRFRPPTNLRSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDV
                                                                                                                                                                                                                                                                                                                                                   AAY70654 standard; Protein; 187 AA.
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                                                                                                                                                                                     KLLLGPNDAPAGP 133
                                                                                                                                                                                                            antiviral; cytostatic
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Human transforming growth factor beta-9; Ztgf beta-9; Alzheimer's disease; neurodegenerative disease; Huntington's disease; amyofrophic lateral sclerosis; ALS; Parkinson's disease; peripheral neuropathy; demyelinating disease; multiple sclerosis; antiviral; cytostatic.
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and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mature human Ztgfbeta-9 variant protein.
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                                                                                                                                                                                                                                                                                                                                                                          AAY70663 standard; Protein; 187
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The present sequence is the mature human transforming growth factor beta-9, designated 2tgf beta-9. This is a mature sequence excluding the signal sequence extending from amino acid 17 to and including amino acid 20.2 of 2tgf beta-9. Human 2tgf beta-9 was isolated from an arrayed pituitary gland cDNA plasmid library by PCR screening. This can be used to treat a variety of neurodegenerative diseases such as amyotrophic lateral sclerosis (ALS), Alzheimer's disease, Huntington's disease, Parkinson's disease and peripheral neuropathies, or demyelinating aliseases including multiple sclerosis. Ztgf beta-9 peptides have antiviral activity and may also be used to regulate the proliferation, differentiation and apoptosis of neurons, glial cells, lymphocytes, hematopoietic cells and stromal cells.
                                                                          RFRSAPVYMPTVVLRRTPACAGGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGA 120
                                                                                                                                                            Mature human transforming growth factor beta-9, Ztgfbeta-9 protein-2.
                                                  1 SCPAGGRPADRRFRPPTNLRSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotides encoding a novel transforming growth factor beta-9 polypeptide, designated Ztgf beta-9, useful as an antiviral and antiproliferative agent -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peripheral neuropathy; demyelinating disease; multiple sclerosis; antiviral; cytostatic.
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100.0%; Score 729; DB 21;
Best Local Similarity 100.0%; Pred. No. 1:3e-74;
Matches 133; Conservative 0; Mismatches 0;
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N-PSDB; AAZ52195.
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Pred. No. 1.3e-74;
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      Pred. No. 1.2e-74;
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                                                                                                                                                                                                                                       121 KLLLGPNDAPAGP 133
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Best Local Similarity
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                       Matches 133;
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Gaps

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The present sequence represents a partial human interleukin-22 (IL-22) protein. The specification also describes IL-21 polynuclectides and polypeptides. The IL-21 polynuclectide was isolated from a cDNA library of epileptic frontal cortex. IL-21 and IL-22 may be useful in treating of ediciencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells, treating or detecting deficiencies of haematopoietic cells, treating or detecting deficiencies of the manacopoietic cells, treating or detecting autoimmune disorders, treating asthma (particularly allergic asthma) or other respiratory problems, to treat and/or prevent organ rejection or graft-versus-host disease (symb), to modulate inflammation, to treat or detect hyperproliferative disorders, to treat or detect infectious agents, to differentiate, proliferate and attract cells, leading to the regeneration of tissues, IL-22 may also increase or decrease the differentiation or proliferation of embryonic stem cells and haematopoietic lineage, may be used to modulate mammalian characteristics.
                                                                                                                                                                                                                        "Asn39 is a potential N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polynucleotides used to develop products for treating e.g. immune disorders, blood disorders, autoimmune disorders, allergies, inflammation, hyperproliferative disorders or infections
              haemostatic activity; thrombolytic activity; autoimmune disorder; asthma respiratory problem; organ rejection; graft-versus-host disease; GVHD; inflammation; hyperproliferative disorder; tissue regeneration; embryonic stem cell differentiation; embryonic stem cell proliferation; haematopoietic lineage; allergic asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Asn152 is a potential N-linked glycosylation
 immune cell chemotaxis; haematopoietic cell disorder;
                                                                                                                                                                                                                                       /note= "conserved domain VII" 69..77
                                                                                                                                                                                                                                                                                                                                                                "conserved domain III"
                                                                                                                                                                                                                                                                                                           85..90
/note= "conserved domain II"
                                                                                                                                                                                        "conserved domain VI"
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                                                                                                                                                     Location/Qualifiers
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98US-0099805.
99US-0131965.
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152..154
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N-PSDB; AAZ36837.
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                                                                                                                                                                                                        Modified-site
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                                                                                                                       Homo sapiens
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                                                                                                                                                           Key
 The present sequence represents a partial human interleukin-22 (IL-22) protein. The specification also describes IL-21 polynucleotides and protein. The specification also describes IL-21 polynucleotide was isolated from a cDNA library of epileptic frontal cortex. IL-21 and IL-22 may be useful in treating confidencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells, treating or detecting deficiencies or disorders of haematopoietic cells, to modulate haemostatic or thrombolytic activity, in treating or detecting autoimmune disorders, treating asthma (particularly allergic asthma) or other respiratory problems, to treat and/or prevent organ rejection or graft-versus-host disease (GVHD), to modulate inflammation, to treat or detect infectious agents, to differentiate, proliferate and attract cells, leading to the differentiate, proliferation of trisates and attract cells, leading to the crease the differentiation or proliferation of embryonic stem cells and characterized to haematopoietic lineage, may be used to modulate mammalian
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                                                                                                                                                                                                                                                                                             Novel polynucleotides used to develop products for treating e.g. immune disorders, blood disorders, autoimmune disorders, allergies, inflammation, hyperproliferative disorders or infections
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; Pred. No. 1.1e-74;
0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 133; Conservative 0.
                                                                                                 98US-0097340.
98US-0099805.
99US-0131965.
                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                  99WO-US11644
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N-PSDB; AAZ36835.
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W09961617-A1
                                                                  27-MAY-1999;
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30-APR-1999;
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Human Human

Perfect score:

Sequence:

protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

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Database

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Human; interleukin-22; IL-22; IL-21; immune system disorder; immune cell chemotaxis; haematopoietic cell disorder; haematopoietic cell disorder; haemostatic activity; thrombolytic activity; autoimmune disorder; asthma; respiratory problem; organ rejection; graft-versus-host disease; GVHD; inflammation; hyperproliferative disorder; tissue regeneration; embryonic stem cell differentiation; embryonic stem cell differentiation; embryonic stem cell proliferation; haematopoietic lineage; allergic asthma.
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AAY44485
AAY70661
AAY44461
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AAW85641
AAW85642
AAW85640
AAW85644
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AAY70657
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AAB07602
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AAW85619
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                         AAB07597
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26
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Human transforming
Human transforming
A human interleuki
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         GenCore version
Copyright (c) 1993 - 2000
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Listing first 45 summaries
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Score

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